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OM protein - protein search, using sw model

Run on: February 16, 2001, 21:03:25 ; Search time 30.21 seconds
(without alignments)
471.990 Million cell updates/sec

Title: us-09-380-276a-4

Perfect score: 2255

Sequence: 1 MALKVLEGEKFTLLVLL.....LDQSGAIHPATQTSLOEA 417

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_36.*

1: /SIDSI/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq/AA1982.DAT.*
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7: /SIDSI/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SIDSI/gcgdata/geneseq/geneseq/AA1988.DAT.*
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11: /SIDSI/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SIDSI/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SIDSI/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SIDSI/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseq/AA1996.DAT.*
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19: /SIDSI/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2246	99.6	417	20 W98146	Human TRAIN-R. Ho
2	2241	99.4	423	20 W85724	Novel protein (C10
3	2239	99.3	417	19 W70386	Amino acid sequenc
4	2230	98.9	423	19 W70387	Amino acid sequenc
5	2221	98.5	423	20 W93581	Human hAPO4-alpha
6	1563.5	69.3	416	20 W93579	Mouse MAP04-alpha
7	1544.5	68.5	328	20 Y06400	Human NTR-5 recept
8	977	43.3	214	20 Y06522	Mouse STRIFE1 (Tan
9	977	43.3	214	20 W98145	Mouse TRAIN-R (lon
10	977	43.3	214	20 W93580	Mouse MAP04-alpha
11	869	38.5	210	20 Y22223	Human TNFR superfa
12	854	37.9	150	20 W98148	TRAIN-R short, sol

13	783	34.7	160	20 Y06399	Mouse NTR-5 recept
14	725	32.2	150	20 Y06523	Mouse STRIFE2 (Tan
15	725	32.2	150	20 Y22224	Mouse TNFR superfa
16	725	32.2	150	20 W98144	Mouse TRAIN-R (Sho
17	725	32.2	150	20 W93583	Mouse MAP04-gamma
18	725	32.2	150	21 Y77465	Murine Rank-like p
19	480	21.3	231	21 Y77468	Human Rank-like pr
20	267.5	11.9	109	20 W93582	Rat rAPO4-alpha pr
21	244	10.8	77	21 Y77467	Human Rank-like pr
22	192.5	8.5	132	21 Y77466	Human Rank-like pr
23	179	7.9	30	20 W98147	TRAIN-R secreted f
24	159	7.1	438	16 R81882	Plasmid pDC406/OX4
25	159	7.1	438	19 W48976	OX40/Fc mutein. C
26	150	6.7	206	16 R81881	Mouse type-II memb
27	150	6.7	206	19 W48977	Mouse OX40 extrace
28	148	6.6	95	20 W93584	Mouse MAP04-beta p
29	146.5	6.5	1801	19 W50895	Rat laminin B2 cha
30	144	6.4	1104	17 R94957	NF-X1 DNA-binding
31	140.5	6.2	408	20 Y41111	Human TANGO 129 (T
32	140.5	6.2	430	20 Y41110	Human TANGO 129 (T
33	140.5	6.2	430	21 Y70785	Human tumour necro
34	140	6.2	425	21 Y92370	p75-NTR (neurotrop
35	136.5	6.1	1798	19 W50896	Human laminin B2 c
36	136	6.0	625	19 W83200	Murine osteoclast
37	136	6.0	625	19 W69958	Murine NF-kB recep
38	136	6.0	625	19 W68294	Murine NF-kB recep
39	136	6.0	625	21 Y59509	OBM binding protei
40	136	6.0	625	21 Y53849	A mouse receptor a
41	134	5.9	186	15 R62655	Cowpox virus pst 1
42	134	5.9	307	18 W33358	TBP(20-161)/hCG-be
43	134	5.9	1764	10 P91672	Primary amino acid
44	134	5.9	1776	19 W50894	Mouse laminin B1 c
45	133.5	5.9	2050	20 W73499	Von Willebrand fac

ALIGNMENTS

RESULT 1
W98146
ID W98146 standard; Protein; 417 AA.
XX
AC W98146;
XX
DT 05-JUL-1999 (first entry)
XX
DE Human TRAIN-R.
XX
KW TRAIN-R; receptor; human; tumour necrosis factor receptor;
KW agonist; antagonist; cancer; immunological disease; therapy;
KW cytostatic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..21 /note= "signal peptide"
FT Protein 22..417 /note= "mature protein"
FT Domain 26..173 /note= "extracellular domain"
FT Domain 174..190 /note= "transmembrane domain"
FT Domain 191..417 /note= "cytoplasmic domain"
XX
PN WO9913078-A1.
XX
PD 18-MAR-1999.
XX
PF 11-SEP-1998; 98WO-US19030.
XX
PR 06-MAY-1998; 98US-0084422.

PR 12-SEP-1997; 97US-0058631.
 XX (BIOJ) BIOGEN INC.
 PA
 PI Hesslon C, Tschopp J;
 XX WPI; 1999-229238/19.
 XX DR N-PSDB; X24978.
 XX
 PT New cysteine-rich tumor necrosis factor receptor
 XX
 PS Claim 2; Page 26; 30pp; English.
 XX
 CC The present sequence is a novel human cysteine-rich tumour
 CC necrosis factor receptor family member termed TRAIN-R that is
 CC expressed at low levels in every tissue and cell line tested thus
 CC far, with higher expression detected in heart, prostate, ovary,
 CC testis, peripheral blood lymphocytes, thyroid and adrenal gland.
 CC Cell death can be induced by administering an agent capable of
 CC inhibiting the binding of TRAIN-R to its ligand. A claimed method
 CC of treating, or reducing, the advancement, severity or effects of
 CC an immunological disease in a mammal comprises administering a
 CC pharmaceutical composition which comprises a TRAIN-R blocking agent,
 CC e.g. soluble TRAIN-R. TRAIN-R can be fused to an immunoglobulin to
 CC produce a fusion protein which may be targeted to various sites.
 CC It can be used in binding assays, and to identify antagonists and
 CC agonists. Anti-TRAIN-R antibodies can be used to reduce the
 CC severity of an immune response or to treat cancer. TRAIN-R
 CC blocking agents can also be used to reduce the severity or effects
 CC of an immunological disease (all claimed).
 XX
 SQ Sequence 417 AA;

Query Match 99.6%; Score 2246; DB 20; Length 417;
 Best Local Similarity 99.3%; Pred. No. 1.1e-199;
 Matches 414; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALKVLEQEKTFETLLVLLGLYSCKVTCTGDCROQEFDRSGNVCVPCNOCQPGMELSK 60
 DB 1 malkvleqektftllvllglyskvtctesgdcrgqefdrsgncvpcnqcpgmelsk 60

QY 61 ECGFGYGEDAQVCTRLHREKEDWGQKCKPCLDCAVNNRFQKANCSDATSAICGDLCPG 120
 DB 61 ecgfygedaqvctrlhrfkedwgqkckpcldcavnnrfqkancsatsdaicgdlcp 120

QY 121 FYRKTILVGFQDMCEVPCGDPGPPPEPHCASKVNLKIASTASSPRDTALAAVICSALAT 180
 DB 121 fyrktlvgfmdmcevcpgdppppphcaskvnlkiasstassprdtalaavicsalat 180

QY 181 VLLALLILCVIYCKRQFMKKPSWLSRSDIOYNGSELSCLDRLPQLHEYAHRACCCRRD 240
 DB 181 vllallilcvyckrfmekkpswlsrsdioxngselcldrpqlheyahraccqrrd 240

QY 241 SVTCGVPVRLPSMCCGEEACSPNATLGCQVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
 DB 241 svtcgvpvrlpsmcceeeacspnatlgcgvhsaaslaqarnagpagemvptffgsltsq 300

QY 301 CGFSDAWPLMQNPMGDDNLSFCDSYPELTGEDIHSLNPELESSTSLDSSODLVGGAV 360
 DB 301 cgfsdawplmqnpgmddnlsfcdsypeeltgedihslnpelesstslsdsodlvvgav 360

QY 361 PVQSHENFTAAATDLRYNNLTVESASTQDALTWRSQDQESCAIITHPATOTSILQEA 417
 DB 361 pvqshenftaatdlrynnltvesastqdaltnrsqldesgavlhpatqtsilqea 417

RESULT 2
 W85724
 ID W85724 standard; Protein: 423 AA.
 XX
 AC W85724;
 XX

DT 27-SEP-1999 (first entry)
 XX
 DE Novel protein (Clone AX92_3).
 XX
 KW Polynucleotide; protein; nutrition; cytokine; cell proliferation;
 KW cell differentiation; immunostimulation; immunosuppression;
 KW haematopoiesis regulation; tissue growth; activin; inhibin;
 KW chemotaxis; chemokinesis; haemostasis; thrombolysis; receptor;
 KW ligand; anti-inflammatory; tumour suppression; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN W09920644-A1.
 PN
 PD 29-APR-1999.
 PD
 XX 16-OCT-1998; 98WO-US22034.
 XX
 PF 18-OCT-1997; 97US-0955557.
 PF
 PR (GEMY) GENETICS INST INC.
 PR
 XX Agostino MJ, Bowman MR, Evans C, Jacobs K, Lavallie ER;
 XX McCoy JM, Merberg D, Racie LA, Spaulding V, Treacy M;
 XX WPI; 1999-288272/24.
 XX
 DR N-PSDB; X08689.
 DR
 XX New polynucleotides encoding secreted human proteins
 XX
 PT Claim 32; Page 117-118; 136pp; English.
 PS
 XX The new human secreted proteins are encoded by polynucleotides
 CC obtained from human placenta, adult testes, fetal kidney, fetal
 CC brain, adult brain, adult brain and adult blood cDNA libraries.
 CC The polynucleotides and proteins are predicted to have biological
 CC activities which would make them suitable for treating, preventing or
 CC ameliorating medical conditions in humans and animals. Suggested
 CC activities include nutritional activity, cytokine and cell
 CC proliferation/differentiation activity, immune stimulating (e.g. as
 CC vaccines) or suppressing activity, haematopoiesis regulating
 CC activity, tissue growth activity, activin/inhibin activity,
 CC chemotactic/chemokinetic activity, haemostatic and thrombolytic
 CC activity, receptor/ligand activity, anti-inflammatory activity,
 CC cadherin/tumour invasion suppressor activity, and tumour inhibition
 CC activity. The polynucleotides are also stated to be useful for gene
 CC therapy. The sequences identified by a secretory leader
 CC sequence motif in the polynucleotide and it is thought that the
 CC encoded proteins have biological activity by virtue of their secreted
 CC nature. This polypeptide was encoded by a clone designated AX92_3
 CC (See X08689).
 XX
 SQ Sequence 423 AA;

Query Match 99.4%; Score 2241; DB 20; Length 423;
 Best Local Similarity 99.8%; Pred. No. 3.2e-199;
 Matches 414; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALKVLEQEKTFETLLVLLGLYSCKVTCTGDCROQEFDRSGNVCVPCNOCQPGMELSK 60
 DB 1 malkvleqektftllvllglyskvtctgdcrgqefdrsgncvpcnqcpgmelsk 60

QY 61 ECGFGYGEDAQVCTRLHREKEDWGQKCKPCLDCAVNNRFQKANCSDATSAICGDLCPG 120
 DB 61 ecgfygedaqvctrlhrfkedwgqkckpcldcavnnrfqkancsatsdaicgdlcp 120

QY 121 FYRKTILVGFQDMCEVPCGDPGPPPEPHCASKVNLKIASTASSPRDTALAAVICSALAT 180
 DB 121 fyrktlvgfmdmcevcpgdppppphcaskvnlkiasstassprdtalaavicsalat 180

QY 181 VLLALLILCVIYCKRQFMKKPSWLSRSDIOYNGSELSCLDRLPQLHEYAHRACCCRRD 240
 DB 181 vllallilcvyckrfmekkpswlsrsdioxngselcldrpqlheyahraccqrrd 240

Db 101 vllallilcivckrqfmeckpwsrlsqdiqngselscldrpqlheyahracccqrrd 240
Qy 241 SVQTCGPVRLLPSCMCEEACSPNPATLCGCVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Db 241 svqtcgprllpsmcceaacspnatlpgcvghsaaslaqarnagpagemvptffgsltsqi 300
Qy 301 CGEFSDAWPLMONGMGNISFCDSYPELTGEDTHSLNPELESSTLSDNSQDLVGGAV 360
Db 301 cgefsdawplmqnpgmgdnisfcdsyplagedihslnpelesstlidsnssqdlvggav 360
Qy 361 PVQSHSENFTATDLRYNNLTVESASTQDALTMRSQDLQESGALIHHPATQTSLSQ 415
Db 361 pvqshsenftaatdlsrynntlivesastqdaltrmsqldqesgalinhpatqtsisq 415
RESULT 3
W70386
ID W70386 standard; Protein; 417 AA.
XX
AC W70386;
XX
DT 02-DEC-1998 (first entry)
XX
DE Amino acid sequence of human alpha-OAF065.
XX
KW Human; alpha-OAF065; stroma cell; antibody; inflammatory;
cystokine-mediated disease; rheumatism; ulcerative colitis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 223
FT /note= "encoded by AGA"
FT Misc-difference 224
FT /note= "encoded by CCT"
XX
FN WO9838304-A1.
XX
PD 03-SEP-1998.
XX
PF 26-FEB-1998; 98WO-JP00799.
XX
PR 27-FEB-1997; 97JP-0043143.
XX
PA (ONOY) ONO PHARM CO LTD.
XX
PI Fukushima D, Konishi M, Tada H;
XX
DR WPI; 1998-481205/41.
DR N-PSDB; V33361.
XX
PT Membrane polypeptide expressed by human stroma cells, and antibodies
recognising it - for treatment of inflammatory and other
cystokine-mediated diseases.
XX
PS Claim 1; Pages 28-30; 54pp; Japanese.
XX
CC This is the amino acid sequence of the human alpha-OAF065, used in
the method of the invention. The process involves the use of peptides
expressed by stroma cells, and its antibodies are used for in the
prevention and treatment of inflammatory and other cytokine-mediated
diseases such as rheumatism, ulcerative colitis.
XX
SQ Sequence 417 AA;
Query Match 99.3%; Score 2239; DB 19; Length 417;
Best Local Similarity 99.5%; Pred. NO. 4.8e-199;
Matches 415; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MALKVLLSEQKTFFTLLVLLGYLSCKVTCETDCRQEFDRSGNVCNCGPGMELSK 60
Db 1 malkvllseqkftfllvllgylsckvtcetdcrqefdrsgnvcncpgpgmeisk 60

Qy 61 ECGFGYGEDAQCVCRLHREKEDMGFOCKPCLDCAVNVNRFQKANCATSDAICGDCLPg 120
Db 61 ecgfygygedaqcvctrlhrfkedwgfckpcldcavvnrfqkancatsdaicgdcclpg 120
Qy 121 FYRKTGLVGFODMECVPCGDPPIPPYEPHCASKVNLVKIATASSPRDTALAAVICSALAT 180
Db 121 fyrktglvfgdmevcpcgdpippiyephcaskvnlvkiastassprdtalaavicsalat 180
Qy 181 VLLALLILCIVCKROFMEKPSWLSRSQDIQYNGSELSCLDROPOLHEYAHRAACOCRRD 240
Db 181 vllallilcivckrqfmeckpwsrlsqdiqngselscldrpqlheyahracccqrrd 240
Qy 241 SVQTCGPVRLLPSCMCEEACSPNPATLCGCVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Db 241 svqtcgprllpsmcceaacspnatlpgcvghsaaslaqarnagpagemvptffgsltsqi 300
Qy 301 CGEFSDAWPLMONGMGNISFCDSYPELTGEDTHSLNPELESSTLSDNSQDLVGGAV 360
Db 301 cgefsdawplmqnpgmgdnisfcdsyplagedihslnpelesstlidsnssqdlvggav 360
Qy 361 PVQSHSENFTATDLRYNNLTVESASTQDALTMRSQDLQESGALIHHPATQTSLSQEA 417
Db 361 pvqshsenftaatdlsrynntlivesastqdaltrmsqldqesgalinhpatqtsisqea 417
RESULT 4
W70387
ID W70387 standard; Protein; 423 AA.
XX
AC W70387;
XX
DT 02-DEC-1998 (first entry)
XX
DE Amino acid sequence of human beta-OAF065.
XX
KW Human; beta-OAF065; stroma cell; antibody; inflammatory;
cystokine-mediated disease; rheumatism; ulcerative colitis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 223
FT /note= "encoded by AGA"
FT Misc-difference 224
FT /note= "encoded by CCT"
XX
FN WO9838304-A1.
XX
PD 03-SEP-1998.
XX
PF 26-FEB-1998; 98WO-JP00799.
XX
PR 27-FEB-1997; 97JP-0043143.
XX
PA (ONOY) ONO PHARM CO LTD.
XX
PI Fukushima D, Konishi M, Tada H;
XX
DR WPI; 1998-481205/41.
DR N-PSDB; V33362.
XX
PT Membrane polypeptide expressed by human stroma cells, and antibodies
recognising it - for treatment of inflammatory and other
cystokine-mediated diseases.
XX
PS Disclosure; Pages 37-49; 54pp; Japanese.
XX
CC This is the amino acid sequence of the human beta-OAF065, used in
the method of the invention. The process involves the use of peptides
expressed by stroma cells, and its antibodies are used for in the
prevention and treatment of inflammatory and other cytokine-mediated
diseases such as rheumatism, ulcerative colitis.
CC

XX PS Sequence 423 AA;

Query Match 98.9%; Score 2230; DB 19; Length 423;
 Best Local Similarity 99.5%; Pred. No. 3.4e-198;
 Matches 413; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MALKVLLQEKEFTFTLLVLLGLYLSCKVTCTGTGDCRQOEFRDRSGNVCPCNQCGPMELSK 60
 |||||
 Db 1 malkvllleqektfftlvlllgylsckvtctgdcrgqefdrsgncvpcnqcgpmelask 60
 |||||

Qy 61 ECGFGYGEDAQCVTCRLHRFKEDWGQKCPCLDCAVVNRFKANCATSDAICGDCPLG 120
 |||||
 Db 61 ecgfygedaqcvtrlhfrkdwgfgkcpcldcavvnrfgkancatsdaicgdcplg 120
 |||||

Qy 121 FYRKTILVGFQDMCEVPCGDPDPPEPHCAKSKVNLVKIASTASSPRDTALAAVICSALAT 180
 |||||
 Db 121 fyrktlilcvtyckrqfmeckpwsrldsqdyngselcldrpqlheyaahracccrrd 180
 |||||

Qy 181 VLLALLILCVYCKRQPMKPSWSLRSDIQYNGSELSCLDRLPQLHEYAHRAACCCRRD 240
 |||||
 Db 181 vllallilcvtyckrqfmeckpwsrldsqdyngselcldrpqlheyaahracccrrd 240
 |||||

Qy 241 SVQTCGVPRLPSCMCCEACSPNPATLGCYVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
 |||||
 Db 241 svqtcgvrllpsmcceacspnpatlgcgvhsaaslqarnagpagemvptffgsltsqi 300
 |||||

Qy 301 CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTLSDNSQDLVGGAV 360
 |||||
 Db 301 cgefsdawplmqnpgmgdnisfcdsytpeltgedihslnpelesstldnsqdlvggav 360
 |||||

Qy 361 PVQSHSENFTAATDLRYNNNTLVESASTQDALTMRSQDQESGAIHPATQTSIQ 415
 |||||
 Db 361 pvqshsenftaatdlsrynnntlvessastqdaltmrsqldqesgailhpatqtsiq 415
 |||||

RESULT 5
 W93581
 ID W93581 standard; Protein; 423 AA.

XX AC W93581;
 XX DT 18-JUN-1999 (first entry).
 XX DE Human hAPO4-alpha protein.
 XX KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
 KW developmental abnormality; gestational abnormality; prostate cancer;
 KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
 KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
 KW apoptosis; human; APO4-alpha.

XX OS Homo sapiens.
 XX PN W09911791-A2.
 XX PD 11-MAR-1999.
 XX PF 04-SEP-1998; 98WO-0518393.
 XX PR 05-SEP-1997; 97US-0924634.
 XX PA (UNIW) UNIV WASHINGTON.
 XX PI Chaudhary PM;
 XX DR WPI; 1999-205191/17.
 XX N-PSDB; X23415.
 XX PT New Tumor Necrosis Factor family receptor polypeptides and ligands -
 PT useful for diagnosis and treatment of prostate cancer and
 PT developmental or gestational abnormalities

KW APO6; APO8; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
 KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
 KW apoptosis; mouse; mAPO4-alpha.

OS Mus sp.

XX WO9911791-A2.

PN 11-MAR-1999.

XX 04-SEP-1998; 98WO-US18393.

XX 05-SEP-1997; 97US-0924634.

XX (UNIW) UNIV WASHINGTON.

PA Chaudhary PM;

PI WPI; 1999-205191/17.

XX N-PSDB; X23413.

XX New Tumor Necrosis Factor family receptor polypeptides and ligands -
 PT useful for diagnosis and treatment of prostate cancer and
 PT developmental or gestational abnormalities

XX Claim I; Fig 7A; 156pp; English.

XX This invention describes isolated Tumor Necrosis Factor (TNF) family
 CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
 CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
 CC their active fragments. APO4 is useful for diagnosing prostate cancer
 CC by determining levels of APO4 in an individual. Prostate cancer can also
 CC be treated using APO4 selective binding agents linked to a therapeutic
 CC moiety. APO4 polypeptides are also useful for identifying selective
 CC binding agents, useful in diagnosis/treatment of disease by binding of
 CC agents to the polypeptide/active fragment which is extracellular, or
 CC expressed on the cell surface. The binding is preferably performed in
 CC vivo. APO4 polypeptides/active fragments are also useful for screening
 CC for agonists and antagonists by binding and observing the change in APO4
 CC activity. Effective pharmacological agents useful in diagnosis or
 CC treatment of disease are also identified using APO4 polypeptides/active
 CC fragments and APO4 signal transducer molecules that specifically interact
 CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
 CC activity. The method is performed in vivo or in vitro. APO polypeptides
 CC are all useful as immunogens for preparing antibodies. APO4 is also
 CC useful for diagnosis/treatment of developmental or gestational
 CC abnormalities. APO8 was transfected to human breast carcinoma cell line
 CC MCF-7, and induced apoptosis.

XX Sequence 416 AA;

Query Match 69.3%; Score 1563.5; DB 20; Length 416;
 Best Local Similarity 70.4%; Pred. No. 1.6e-136;
 Matches 295; Conservative 34; Mismatches 85; Indels 5; Gaps 3;

QY 1 MALKVLEGEKFTFTLLVLLGSKVTCTGTCROEPRDRSGNVCPCNQCPCGMELSK 60
 Db 1 malkvlphrtvlfaiillhlackvscetgdcrgqefkdrsgncvclkcqgpgmelsk 60
 QY 61 ECGFGYGEDAQCVTCRLHFKEDWQKCKPCLDCAVNRFRKANCATSIDAICGDCPLG 120
 Db 61 ecgfygedaqcvpcrphrfkdwgfkckpcadcalvnrfrancshcsdavgdcplg 120
 QY 121 FYRKTLYGFDQMECYPCGDPPEPHCASKVNLVKIATSSPRDPTALAAVICSALAT 180
 Db 121 fyrtklyvgfdqmevcygcgdppephcaskvnlvkiatssvprdtalaavicsalat 180
 QY 181 VLLALITLCVYCKROFMKKPSWSLRSDIOVNGSELSCLDRLPQLHEVHRAACCCRRD 240
 Db 181 vllallilvcyckrfmekkpswslrsqdiqngselscfcdqprlrhcacccqyhrd 240
 QY 241 SVOTCGFVRLPLSMCCEACSPNATLGCVGVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300

Db 241 sapmygpvhlpisclceearsaravlgclrspttlqernpasvgnmtmpaffgsvsrsi 300
 QY 301 CGEFSDAWPLMONGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSQDLVGGAV 360
 Db 301 caefsdawplmgnp19gds-sicdsypeltdetnslnpenestslsdsgsgqdlagta- 358
 QY 361 PVQSHSENFATDLSRYNN--TLVESASTQDALTMRSQDQESGAIHHPATQTSIQEA 417
 Db 359 -alessgnvsestdsprhgdgtgtvweqlaqdqrtpsggwdrenlnlampaifqda 416

RESULT 7

Y06400

ID Y06400 standard; Protein; 328 AA.

XX AC Y06400;

XX 20-SEP-1999 (first entry)

DT Human NTR-5 receptor.

DE NTR-5; human; receptor; signal transduction; bone; muscle;

KW diagnosis; therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..29

FT Protein /note= "signal peptide"

FT Domain /note= "mature protein"

FT Domain /note= "extracellular domain"

FT Domain /note= "transmembrane domain"

FT Domain /note= "intracellular domain"

XX WO95333967-A2.

XX 08-JUL-1999.

XX 28-DEC-1998; 98WO-US27688.

XX 29-DEC-1997; 97US-0068925.

XX (REGE-) REGENERON PHARM INC.

XX Valenzuela DM;

XX WPI; 1999-419102/35.

XX N-PSDB; X59346.

XX New mammalian receptor NTR-5 polypeptides

XX Claim 7; Page 21-22; 27pp; English.

CC The present sequence represents a novel human receptor, designated
 CC NTR-5, that shows homology to osteoprotegerin and to tumour necrosis
 CC factor receptor. The sequence was predicted from an isolated cDNA
 CC clone (see X59346). Homology to osteoprotegerin suggests that NTR-5
 CC is involved in the regulation of bone mass, and may be useful for
 CC regulating development, proliferation and death of osteoblast or
 CC osteoclast cells or, regulating muscle metabolism, and that it
 CC may be implicated in muscle diseases or disorders. A host-vector
 CC system for production of NTR-5 is claimed. NTR-5 polypeptides can
 CC be used as immunogens and in screening assays to identify NTR-5
 CC ligands, agonists and antagonists. Polypeptides comprising the
 CC extracellular domain of NTR-5 fused to an immunoglobulin constant
 CC region, especially to a human immunoglobulin gamma-1 Fc region,
 CC are claimed. The invention also provides for diagnostic and
 CC therapeutic methods based on the interaction of NTR-5 and agents

CC that initiate signal transduction through binding to NTR-5.

XX
XX
SQ Sequence 328 AA;

Query Match 68.5%; Score 1544.5; DB 20; Length 328;
Best Local Similarity 90.2%; Pred. No. 6.5e-135;
Matches 286; Conservative 4; Mismatches 14; Indels 13; Gaps 3;

QY 1 MALKVLEQEKTEFTLLVLLGYLSCKVTCTGTGDCRQOEFDRSGNCVPCNOCQPGWELSK 60
|||||
Db 1 malkvleqektftllvllgylsckvtctgtgdrsgncvpcncqpgwelmelsk 60
|||||

QY 61 ECGFGYGEDAQCVTCRLHREKEDWGFKCKPCLDCAVVRFOKANGCSATSDAICGDLPG 120
|||||
Db 61 ecgfgygedaqcvtrlhrekdwgfqckpcldcavvrfoqkancsatsdaicgdlpg 120
|||||

QY 121 FYRKTLLVGFQDMCEVPCGDPPEPHCHASKVNLVKIATASPRDTALAAVICSALAT 180
|||||
Db 121 fyrktllvgfmdmcevcpgdpppephcaskvnlvkiatassprdtalaavicsalat 180
|||||

QY 181 VLLALLILCVYCKRQFMKKPSWSLRSODIOYNGSELCLDRPOLHEVAHRACCOCRRD 240
|||||
Db 181 vllallilcvyckrfmekkpswsrslrsodioyngselcldrpolhevaahraccocrrd 240
|||||

QY 241 SVQTCGPVRLPSMCCCEACSPNATLGCYVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
|||||
Db 241 svqtcgpvrllpsmccceacspnatlgcgvhsaaslqarnagpagemvptffgsltqsi 300
|||||

QY 301 CGEFSADWPLQNPMDG 317
| | | | |
Db 294 c-----wnpkstpllg 304

RESULT 8
Y06522
ID Y06522 standard; Protein; 214 AA.
AC Y06522;
DT 08-OCT-1999 (first entry)
XX Mouse STRIFE1 (Tango 127a) TNF receptor.
DE
KW STRIFE1; Tango 127a; mouse; tumour necrosis factor receptor;
KW sepsis; circulatory collapse; toxic shock; infection;
KW immune disease; autoimmune disease; alcohol-induced hepatitis;
KW inflammation; graft versus host pathology; cancer; tumour;
KW cerebral malaria; multiple sclerosis; diagnosis; therapy.
XX Mus musculus.
XX
XX Key Location/Qualifiers
FT Peptide 1..29
FT Protein /note= "signal peptide"
FT Protein 30..214
FT Domain /note= "mature protein"
FT Domain 34..72
FT Domain /note= "cysteine-rich domain"
FT Domain 75..114
FT Domain /note= "cysteine-rich domain"
FT Domain 169..193
FT Domain /note= "transmembrane domain"
XX WO9937818-A1.
XX
XX 29-JUL-1999.
XX
XX 27-JAN-1999; 99WO-0501679.
XX
XX 27-JAN-1998; 98US-0014195.
XX
XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX
PI
XX
DR
DR N-PSDB; X87394.
XX
PT New STRIFE1 and STRIFEII polypeptides, proteins and nucleic acid
molecules useful for modulating TNFR associated disorders
XX
PS Claim 26; Fig 1A-B; 119pp; English.
XX
CC The present sequence represents mouse STRIFE1 (also called Tango
127a or T127a), a novel member of the tumour necrosis factor
receptor (TNFR) superfamily. 2 Splice forms of murine STRIFE have
been identified, one that is predicted to be membrane-bound
(STRIFE1) and one that is secreted (STRIFE2, see Y06523). STRIFE
was identified as a TNFR homologue by a computer-based search of
EST databases. The invention provides STRIFE1 and STRIFE2
polynucleotides and polypeptides, fusion proteins, antigenic
peptides and antibodies. It also provides expression vectors,
host cells and transgenic animals, as well as diagnostic, screening
and therapeutic methods. STRIFE I and STRIFE II may play a role in
mediating inflammatory, immune and host defense functions and may
play a role in various neoplastic disease states. They may be
useful as targets for developing novel diagnostic and therapeutic
agents for TNF- and TNFR-associated disorders such as sepsis
syndrome, circulatory collapse and shock resulting from bacterial
infection, acute and chronic parasitic or infectious processes,
acute and chronic immune and autoimmune pathologies, alcohol-induced
hepatitis, chronic inflammatory pathologies, vascular inflammatory
pathologies, graft-versus-host pathology, malignant pathologies
involving TNF-secreting tumors, cerebral malaria and multiple
sclerosis.
XX
SQ Sequence 214 AA;

Query Match 43.3%; Score 977; DB 20; Length 214;
Best Local Similarity 84.6%; Pred. No. 1.2e-82;
Matches 176; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

QY 1 MALKVLEQEKTEFTLLVLLGYLSCKVTCTGTGDCRQOEFDRSGNCVPCNOCQPGWELSK 60
|||||
Db 1 malkvleqektftllvllgylsckvtctgtgdrsgncvpcncqpgwelmelsk 60
|||||

QY 61 ECGFGYGEDAQCVTCRLHREKEDWGFKCKPCLDCAVVRFOKANGCSATSDAICGDLPG 120
|||||
Db 61 ecgfgygedaqcvtrlhrekdwgfqckpcldcavvrfoqkancsatsdaicgdlpg 120
|||||

QY 121 FYRKTLLVGFQDMCEVPCGDPPEPHCHASKVNLVKIATASPRDTALAAVICSALAT 180
|||||
Db 121 fyrktllvgfmdmcevcpgdpppephcaskvnlvkiatassprdtalaavicsalat 180
|||||

QY 181 VLLALLILCVYCKRQFMKKPSWSLRS 208
|||||
Db 181 vllallilcvyckrfmekkpskslrs 208
|||||

RESULT 9
W98145
ID W98145 standard; Protein; 214 AA.
XX
XX W98145;
XX
XX 05-JUL-1999 (first entry)
XX
XX Mouse TRAIN-R (long form).
XX
XX TRAIN-R; receptor; mouse; tumour necrosis factor receptor;
KW agonist; antagonist; cancer; immunological disease; therapy;
KW cytostatic.
XX
XX Mus musculus.
OS

```
xx WO9913078-A1.
pn 18-MAR-1999.
xx
xx 11-SEP-1998; 98WO-US19030.
xx
xx 06-MAY-1998; 98US-0084422.
xx 12-SEP-1997; 97US-0058631.
xx
xx (BIOJ ) BIOGEN INC.
xx
xx Hession C, Tschopp J;
xx
xx WPI; 1999-229238/19.
xx N-PSDB; X24977.
xx
xx New cysteine-rich tumor necrosis factor receptor
xx
xx Claim 2; Page 26; 30pp; English.
xx
xx The present sequence is a novel murine cysteine-rich tumour
xx necrosis factor receptor family member termed TRAIN-R (long form).
xx TRAIN-R is expressed at high levels in murine brain and lung, and
xx at lower levels in liver, skeletal muscle and kidney. Cell death
xx can be induced by administering an agent capable of inhibiting the
xx binding of TRAIN-R to its ligand. A claimed method of treating, or
xx reducing, the advancement, severity or effects of an immunological
xx disease in a mammal comprises administering a pharmaceutical
xx composition which comprises a TRAIN-R blocking agent, e.g. soluble
xx TRAIN-R (see W98144). TRAIN-R can be fused to an immunoglobulin
xx molecule to produce a fusion protein which may be targeted to
xx various sites. It can be used in binding assays, and to identify
xx antagonists and agonists. Anti-TRAIN receptor antibodies can be
xx used to reduce the severity of an immune response or to treat cancer.
xx TRAIN-R blocking agents can be used to reduce the severity or effects
xx of an immunological disease (all claimed).
xx
xx Sequence 214 AA;
xx
xx Query Match 43.3%; Score 977; DB 20; Length 214;
xx Best Local Similarity 84.6%; Pred. No. 1.2e-82;
xx Matches 176; Conservative 10; Mismatches 22; Indels 0; Gaps 0;
xx
xx Qy 1 MALKVLEQEKTFFTLLVLLGYLSCKVTCETGDCRQEQFRDRSGNCVPCNOCQPGMELSK 60
xx Db 1 malkvlphtvtlfaailflhlackvscetgdcrgqefkdrsgncvickqcgpgmelsk 60
xx
xx Qy 61 ECGFGYGEDAQCVTCRLHRFKEDWGFQCKPCLDCAVNVNRFQKANCATSATSDAICGDCLPG 120
xx Db 61 ecgfygedaqcvpcrphrfkdwgfqckpcadcalvnrfgrancshtsdavgcdclpg 120
xx
xx Qy 121 FYRKTKLVGFQDMECVPCGDDPPPPPEPHPCASKVNLVKLTASTASSPRDTALAANVICSALAT 180
xx Db 121 fyrtklvlgfmdmecvpcgddpppppephctskvnlvkisstvssprdtalaavicsalat 180
xx
xx Qy 181 VLLALLILCVYCKRQFMKPSWSLRS 208
xx Db 181 vllallilcvyckrqfmeckpscklps 208
xx
xx RESULT 10
xx ID W93580
xx AC W93580;
xx XX W93580;
xx XX 18-JUN-1999 (first entry)
xx DE Mouse mAPO4-alpha (short) protein.
xx KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
```

```
developmental abnormality; gestational abnormality; prostate cancer;
APO6; APO8; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
apoptosis; mouse; mAPO4-alpha.
Mus sp.
WO9911791-A2.
11-MAR-1999.
04-SEP-1998; 98WO-US18393.
05-SEP-1997; 97US-0924634.
(UNIW ) UNIV WASHINGTON.
Chaudhary PM;
WPI; 1999-205191/17.
N-PSDB; X23414.
New Tumor Necrosis Factor family receptor polypeptides and ligands -
useful for diagnosis and treatment of prostate cancer and
developmental or gestational abnormalities
Claim 1; Fig 7B; 156pp; English.
This invention describes isolated Tumor Necrosis Factor (TNF) family
receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
their active fragments. APO4 is useful for diagnosing prostate cancer
by determining levels of APO4 in an individual. Prostate cancer can also
be treated using APO4 selective binding agents linked to a therapeutic
moiety. APO4 polypeptides are also useful for identifying selective
binding agents, useful in diagnosis/treatment of disease by binding of
agents to the polypeptide/active fragment which is extracellular, or
expressed on the cell surface. The binding is preferably performed in
vivo. APO4 polypeptides/ active fragments are also useful for screening
for agonists and antagonists by binding and observing the change in APO4
activity. Effective pharmacological agents useful in diagnosis or
treatment of disease are also identified using APO4 polypeptides/active
fragments and APO4 signal transducer molecules that specifically interact
with a cytoplasmic domain of APO4 and detecting a change in level of APO4
activity. The method is performed in vivo or in vitro. APO polypeptides
are all useful as immunogens for preparing antibodies. APO4 is also
useful for diagnosis/treatment of developmental or gestational
abnormalities. APO8 was transfected to human breast carcinoma cell line
MCF-7, and induced apoptosis.
Sequence 214 AA;
Query Match 43.3%; Score 977; DB 20; Length 214;
Best Local Similarity 84.6%; Pred. No. 1.2e-82;
Matches 176; Conservative 10; Mismatches 22; Indels 0; Gaps 0;
Qy 1 MALKVLEQEKTFFTLLVLLGYLSCKVTCETGDCRQEQFRDRSGNCVPCNOCQPGMELSK 60
Db 1 malkvlphtvtlfaailflhlackvscetgdcrgqefkdrsgncvickqcgpgmelsk 60
Qy 61 ECGFGYGEDAQCVTCRLHRFKEDWGFQCKPCLDCAVNVNRFQKANCATSATSDAICGDCLPG 120
Db 61 ecgfygedaqcvpcrphrfkdwgfqckpcadcalvnrfgrancshtsdavgcdclpg 120
Qy 121 FYRKTKLVGFQDMECVPCGDDPPPPPEPHPCASKVNLVKLTASTASSPRDTALAANVICSALAT 180
Db 121 fyrtklvlgfmdmecvpcgddpppppephctskvnlvkisstvssprdtalaavicsalat 180
Qy 181 VLLALLILCVYCKRQFMKPSWSLRS 208
Db 181 vllallilcvyckrqfmeckpscklps 208
```

Matches	154;	Conservative	11;	Mismatches	19;	Indels	0;	Gaps	
QY	1	MALKVLLLEQEKTEFTLLVLLGYLSCKVTCETGDCRQEQFRDRSGNCVPCNQCGPMELSK	60						
			1	:	:	:	:		
Db	1	malvkplhrvtlfaailflhlackvscetgdcrgqefkdrsgncvltkqcgpgmelsk	60						
QY	61	ECGFGYGEDAQCVTCRLHRPKEDWGQKCKPCLDCAVVNRFQKANGSATSDAICGDCCLPG	120						
			1	:	:	:	:		
Db	61	ecgfygedaqcvpcprhfrkcdwfgqckpcadcalvnrfgancshtsdavcgdcclpg	120						
QY	121	FYRKTKLVGFQDMECVPCGPPPPYPHCAASKVNLVKIASTASSPRDTALAAVICSALAT	180						
			1	:	:	:	:		
Db	121	fyrtkklvgfdmecnvpcgppppyphephtcsknlvklstsvsrdtavaavicsalat	180						
QY	181	VLLA 184							
Db	181	vlla 184							
RESULT	12								
W98148		ID	W98148	standard; Peptide; 150 AA.					
XX	XX	AC	XX	W98148;					
XX	XX		XX						
DT	DT		XX	05-JUL-1999 (first entry)					
DE	DE		XX	TRAIN-R short, soluble form.					
XX	XX		XX	TRAIN-R; receptor; human; tumour necrosis factor receptor;					
KW	KW		XX	agonist; antagonist; cancer; immunological disease; therapy;					
KW	KW		XX	cytostatic.					
XX	XX		XX						
OS	OS		XX	Homo sapiens.					
PN	PN		XX	W09913078-A1.					
PD	PD		XX	18-MAR-1999.					
PF	PF		XX	11-SEP-1998; 98WO-US19030.					
PR	PR		XX	06-MAY-1998; 98US-0084422.					
PR	PR		XX	12-SEP-1997; 97US-0058631.					
PA	PA		XX	(BIOJ) BIOGEN INC.					
XX	XX		XX	Hession C, Tschopp J;					
PI	PI		XX	WPI; 1999-229238/19.					
DR	DR		XX	New cysteine-rich tumor necrosis factor receptor					
PS	PS		XX	Disclosure; Page 28; 30pp; English.					
XX	XX		XX						
CC	CC		CC	The present sequence comprises the putative short, secreted soluble					
CC	CC		CC	form of a novel human cysteine-rich tumour necrosis factor receptor					
CC	CC		CC	family member termed TRAIN-R. The sequence was produced from a					
CC	CC		CC	30-amino acid peptide (see W98147) encoded by a cloned exon					
CC	CC		CC	sequence (see X24579) and by comparison to the murine TRAIN-R					
CC	CC		CC	short form (see W98144). The human soluble TRAIN-R protein is					
CC	CC		CC	expected to inhibit signalling by full-length human TRAIN-R (see					
CC	CC		CC	W98146). Human TRAIN-R is expressed at low levels in every tissue					
CC	CC		CC	and cell line tested thus far, with higher expression detected in					
CC	CC		CC	heart, prostate, ovary, testis, peripheral blood lymphocytes,					
CC	CC		CC	thyroid and adrenal gland. Cell death can be induced by					
CC	CC		CC	administering an agent capable of inhibiting the binding of TRAIN-R					
CC	CC		CC	to its ligand. A claimed method of treating, or reducing, the					
CC	CC		CC	advancement, severity or effects of an immunological disease in a					
CC	CC		CC	mammal comprises administering a pharmaceutical composition which					
CC	CC		CC	comprises a TRAIN-R blocking agent, e.g. soluble TRAIN-R. TRAIN-R					
CC	CC		CC	can be fused to an immunoglobulin to produce a fusion protein which					
CC	CC		CC	may be targeted to various sites. It can be used in binding assays,					
CC	CC		CC	and to identify antagonists and agonists. Anti-TRAIN-R antibodies.					

CC can be used to reduce the severity of an immune response or to treat
CC cancer. TRAIN-R blocking agents can also be used to reduce the
CC severity or effects of an immunological disease (all claimed).
XX
SQ Sequence 150 AA;

Query Match 37.9%; Score 854; DB 20; Length 150;
Best Local Similarity 99.3%; Pred. No. 1.7e-71;
Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MALKVLLDQEKTFLLVLLGLSKVTCETGDCRQQRDRSGNCVPCNCGGPMELSK 60
|||||
Db 1 malkvillegektffllvllgysckvtcesgdcqrqqrdrsgncvpcnccgpgmelsk 60
|||||
Qy 61 ECGFGYGDAQCVCRLHREFKEDWGFKCKPCLDCAVNNRFQKNCATSDAICGDCPLG 120
|||||
Db 61 ecgfyggedaqcvcrtlhrfkdwgfkckpcldcavnnrfqkncatsdaicgdcplg 120
|||||
Qy 121 FYRKTLYGFQDMECVPCGDPDPPEPHC 149
|||||
Db 121 fyrrtklvgfdmecnvpcgdpdppephc 149

RESULT 13
Y06399
ID Y06399 standard; Protein; 160 AA.
AC Y06399;
XX
XX Y06399;

DT 20-SEP-1999 (first entry)
DE Mouse NTR-5 receptor.
XX
XX NTR-5: mouse; receptor; signal transduction; bone; muscle;
KW diagnosis; therapy.
KW
XX

OS Mus musculus.
XX
XX WO9933967-A2.
XX
PD 08-JUL-1999.
XX
XX 28-DEC-1998; 98WO-US27688.
XX
XX 29-DEC-1997; 97US-0068925.
XX
XX (REGE-) REGENERON PHARM INC.
XX

PI Valenzuela DM;
XX
XX WPI; 1999-419102/35.
DR N-PSDB; X59345.
XX
XX New mammalian receptor NTR-5 polypeptides

PS Example 1; Page 19; 27pp; English.
XX
XX

CC The present sequence represents a novel murine receptor, designated
CC NTR-5, that shows homology to osteoprotegerin and to tumour necrosis
CC factor receptor. The sequence was predicted from isolated cDNA
CC clones (see X59345). Human NTR-5 has also been identified (see
CC Y06400). Homology to osteoprotegerin suggests that NTR-5 is
CC involved in the regulation of bone mass, and may be useful for
CC regulating development, proliferation and death of osteoblast or
CC osteoclast cells or for regulating muscle metabolism, and that it
CC may be implicated in muscle diseases or disorders. A host-vector
CC system for production of NTR-5 is claimed. NTR-5 polypeptides can
CC be used as immunogens and in screening assays to identify NTR-5
CC ligands, agonists and antagonists. The invention also provides for
CC diagnostic and therapeutic methods based on the interaction of
CC NTR-5 and agents that initiate signal transduction through binding
CC to NTR-5.

XX
SQ Sequence 160 AA;

Query Match 34.7%; Score 783; DB 20; Length 160;
Best Local Similarity 91.6%; Pred. No. 7e-65;
Matches 141; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
Qy 55 GMEISKEGFGYGDAQCVCRLHREFKEDWGFKCKPCLDCAVNNRFQKNCATSDAIC 114
|||||
Db 1 gmeiskegfyggedaqcvcprphrfkdwgfkckpcadcalvnnrfqncshsdcavc 60
|||||
Qy 115 GDCLPFGFYRKTLYGFQDMECVPCGDPDPPEPHCASKVNNLVKIASTASSPRDTALAAYI 174
|||||
Db 61 gdcplpgfyrrtklvgfdmecnvpcgdpdppephctskvnlvkiisstvsprdtalaavi 120
|||||
Qy 175 CSALATVLLALLILCVIYCKRQFMFKKPSWSLRS 208
|||||
Db 121 csalatvllallilcvlyckrgfmekpckpsklps 154

RESULT 14
Y06523
ID Y06523 standard; Protein; 150 AA.
XX
XX Y06523;
XX
XX Y06523;

DT 08-OCT-1999 (first entry)
DE Mouse STRIFE2 (Tango 127b) TNF receptor.
XX
XX STRIFE2; Tango 127b; mouse; tumour necrosis factor receptor;
KW sepsis; circulatory collapse; toxic shock; infection;
KW immune disease; autoimmune disease; alcohol-induced hepatitis;
KW inflammation; graft versus host pathology; cancer; tumour;
KW cerebral malaria; multiple sclerosis; diagnosis; therapy.
XX
XX Mus musculus.

Key Location/Qualifiers
FT Peptide 1..29 /note= "signal peptide"
FT Protein 30..150 /note= "mature protein"
FT Domain 34..72 /note= "cysteine-rich domain"
FT Domain 75..114 /note= "cysteine-rich domain"
XX
XX WO9937818-A1.
XX
XX 29-JUL-1999.
XX
XX 27-JAN-1999; 99WO-US01679.
XX
XX 27-JAN-1998; 98US-0014195.
XX
XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
XX Busfield SJ;
XX
XX WPI; 1999-458707/38.
DR N-PSDB; X87395.
XX
XX New STRIFE1 and STRIFEII polypeptides, proteins and nucleic acid
PT molecules useful for modulating TNFR associated disorders
XX
XX Claim 26; Fig 2; 119pp; English.

CC The present sequence represents mouse STRIFE2 (also called Tango
CC 127b or T127b), a novel member of the tumour necrosis factor
CC receptor (TNFR) superfamily. 2 Splice forms of murine STRIFE have
CC been identified, one that is predicted to be membrane-bound

CC (STRIFE1, see Y06522) and one that is secreted (STRIFE2). STRIFE
CC was identified as a TNFR homologue by a computer-based search of
CC EST databases. The invention provides STRIFE1 and STRIFE2
CC polynucleotides and polypeptides, fusion proteins, antigenic
CC peptides and antibodies. It also provides expression vectors,
CC host cells and transgenic animals, as well as diagnostic, screening
CC and therapeutic methods. STRIFE I and STRIFE II may play a role in
CC mediating inflammatory, immune and host defense functions and may
CC play a role in various neoplastic disease states. They may be
CC useful as targets for developing novel diagnostic and therapeutic
CC agents for TNF- and TNFR-associated disorders such as sepsis
CC syndrome, circulatory collapse and shock resulting from bacterial
CC infection, acute and chronic parasitic or infectious processes,
CC acute and chronic immune and autoimmune pathologies, alcohol-induced
CC hepatitis, chronic inflammatory pathologies, vascular inflammatory
CC pathologies, graft-versus-host pathology, malignant pathologies
CC involving TNF-secreting tumors, cerebral malaria and multiple
CC sclerosis.
XX
SQ Sequence 150 AA;

Query Match 32.2%; Score 725; DB 20; Length 150;
Best Local Similarity 82.6%; Pred. No. 1.5e-59;
Matches 123; Conservative 9; Mismatches 17; Indels 0; Gaps 0;
QY 1 MALKVLEQEKFTFTLLVLLGYLSCKVTCGTGCRQEFDRSGNCVPCNQCPCGHELSK 60
DB 1 malkvplhrtvlfafllhllackvscetgdcrgqefkdrsgncvckqcgpgmeisk 60
QY 61 ECGFGYGEDAQCVTCRLHRFKEDWGQKCKPCLDCAVNRFRKANGSATSDAICGDLPG 120
DB 61 ecgfygedaqcvpcprhrfkedwgfgkckpcadcalvnfrqancshsdtavcgdcplg 120
QY 121 FYRKTklvgfQDMECVPCGDPpppppEPhc 149
DB 121 fyrktklvgfQDMECVPCGDPpppppEPhc 149

RESULT 15
Y22224
ID Y22224 standard; Protein; 150 AA.
AC Y22224;
DT 16-SEP-1999 (first entry)
XX Mouse TNFR superfamily soluble receptor protein sequence.
XX TNFL1; human; TNFR superfamily; tumour necrosis factor ligand; TNF;
KW tumour necrosis factor receptor; TNFR superfamily; cell proliferation;
KW cell differentiation; cytokine production; immunoglobulin; hyperplasia;
KW apoptosis inducer; activated T cell; autoimmune disease; inhibitor;
KW myasthenia gravis; insulin-dependent diabetes mellitus; endotoxin shock;
KW rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;
KW tumour; proliferative disorder; neoplasia; dysplasia; immunocompetence;
KW lymphoid organogenesis; bacterial resistance; contact hypersensitivity;
KW delayed type sensitivity; therapy.
XX
OS Mus sp.
XX
XX WO9933980-A2.
XX
XX 08-JUL-1999.
XX
XX 22-DEC-1998; 98WO-0527474.
XX
XX 16-DEC-1998; 98US-0212270.
XX
XX 30-DEC-1997; 97US-0068959.
XX
XX (CHIR) CHIRON CORP.
XX
XX Kassam A, Lamson G, Pot D, Tribouley C;

XX WPI; 1999-405508/34.
DR N-PSDB; X84623.
XX New tumour necrosis factor ligands, useful for induction of cell
PT death and/or proliferation of cells
XX
PS Claim 13; Page 62-63; 69pp; English.
XX
CC This sequence represents a tumour necrosis factor receptor (TNFR)
CC superfamily soluble protein of the invention. The invention also relates
CC to tumour necrosis factor (TNF) ligand (TNFL) family proteins. The TNFL
CC proteins play regulatory roles in cell proliferation and/or
CC differentiation, e.g. they can induce production of cytokines,
CC immunoglobulins, etc. A variety of diseases can be treated by modulating
CC the activity of TNFL proteins, e.g. they can induce apoptosis of
CC activated T cells but rescue resting T cell from apoptosis. TNFL
CC polypeptides can therefore be used to treat autoimmune diseases, such as
CC myasthenia gravis, insulin-dependent diabetes mellitus, rheumatoid
CC arthritis, multiple sclerosis, and systemic lupus erythematosus. TNFL
CC proteins also have tumour stimulating properties, so tumours can be
CC treated by inhibiting the expression or activity of TNFL. Other
CC proliferative disorders, such as neoplasias, dysplasias, and hyperplasia
CC can also be treated using TNFL inhibitors. The TNFL polypeptides and
CC polynucleotides can also be used to enhance or decrease TNF activity,
CC thus providing therapeutic benefits such as induction of cell death,
CC lymphoid organogenesis, or host bacterial resistance, and inhibition of
CC endotoxin shock, contact hypersensitivity, delayed type sensitivity or
CC immunocompetence of a transplant recipient. TNF and its receptors play a
CC major role in host defence and immunosurveillance. As such, there is a
CC need to identify new members of TNFR families. This invention provides
CC this need.
XX
SQ Sequence 150 AA;

Query Match 32.2%; Score 725; DB 20; Length 150;
Best Local Similarity 82.6%; Pred. No. 1.5e-59;
Matches 123; Conservative 9; Mismatches 17; Indels 0; Gaps 0;
QY 1 MALKVLEQEKFTFTLLVLLGYLSCKVTCGTGCRQEFDRSGNCVPCNQCPCGHELSK 60
DB 1 malkvplhrtvlfafllhllackvscetgdcrgqefkdrsgncvckqcgpgmeisk 60
QY 61 ECGFGYGEDAQCVTCRLHRFKEDWGQKCKPCLDCAVNRFRKANGSATSDAICGDLPG 120
DB 61 ecgfygedaqcvpcprhrfkedwgfgkckpcadcalvnfrqancshsdtavcgdcplg 120
QY 121 FYRKTklvgfQDMECVPCGDPpppppEPhc 149
DB 121 fyrktklvgfQDMECVPCGDPpppppEPhc 149

Search completed: February 16, 2001, 21:06:00
Job time: 155 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 16, 2001, 21:04:15 ; Search time 31.47 Seconds
(without alignments)
899.732 Million cell updates/sec

Title: US-09-380-276A-4
Perfect score: 2255
Sequence: 1 MALKVLEQETFTLLVLL.....LDQSGAIHPATQSLQEA 417

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_66:*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	157	7.0	454	1 GOMST1	tumor necrosis fac
2	157	7.0	454	2 I57826	tumor necrosis fac
3	147	6.5	416	1 JN0006	nerve growth facto
4	147	6.5	1797	2 A55677	laminin beta-2 cha
5	146.5	6.5	1801	1 MMRTS	tumor necrosis fac
6	145.5	6.5	435	2 I54182	OX40 antigen precu
7	145	6.4	271	2 S12783	gene ox40 protein
8	144	6.4	272	2 I48700	transcription fact
9	144	6.4	1104	2 I38869	tumor necrosis fac
10	141.5	6.3	461	1 GQRT11	nerve growth facto
11	140	6.2	425	1 A26431	laminin beta-1 cha
12	134	5.9	1786	1 MMMS91	von Willebrand fac
13	133.5	5.9	2813	1 VWHU	thrombospondin 1 p
14	132.5	5.9	1170	2 A40558	B-cell activation
15	132	5.9	277	2 A60771	laminin beta-2 cha
16	129.5	5.7	1798	2 S53869	t2 protein - myxom
17	129	5.7	326	1 GQVZML	thrombospondin 1 p
18	128.5	5.7	1170	1 TSHUP1	dominant autoantig
19	127	5.6	1650	2 S53457	hypothetical prote
20	127	5.6	1827	2 T34288	gp330 protein prec
21	127	5.6	4660	2 T42737	serine proteinase
22	125.5	5.6	1548	2 S34593	laminin B2t chain
23	124.5	5.5	1111	2 B44018	laminin B2t chain
24	124.5	5.5	1193	2 A44018	laminin alpha-1 ch
25	124.5	5.5	3712	2 S18253	G2R protein - vari
26	124	5.5	349	2 D72175	furin (EC 3.4.21.7
27	123	5.5	837	2 S43656	furin (EC 3.4.21.7
28	122	5.4	1299	2 T43231	gene G4R protein -
29	121	5.4	349	2 D36858	

ALIGNMENTS

RESULT 1

GOMST1

tumor necrosis factor receptor 1 precursor - mouse

N:Alternate names: tumor necrosis factor receptor, 55K

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1992 #sequence.revision 30-Jun-1992 #text_change 22-Jun-1999

C:Accession: A38634; B40254; S16677; S19021; I54532

R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991

A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto

A:Reference number: A38634; MUID:91187885

A:Accession: A38634

A:Molecule type: mRNA

A:Residues: 1-454 <LEW>

R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, R.; Brannan, C.I.; Copeland, N.G.; J Mol. Cell. Biol. 11, 3020-3026, 1991

A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f

A:Reference number: A40254; MUID:91246168

A:Accession: B40254

A:Molecule type: mRNA

A:Residues: 1-454 <G02>

A:Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826

R:Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissoneghis, A.M.; Gray, P.W.; Fel Eur. J. Immunol. 21, 1649-1656, 1991

A:Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necro

A:Reference number: S16677; MUID:91285014

A:Accession: S16677

A:Molecule type: mRNA

A:Residues: 1-454 <BAR>

A:Cross-references: EMBL:X59238; NID:g53578; PIDN:CAA41922.1; PID:g53579

R:Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W. Immunogenetics 34, 338-340, 1991

A:Title: Molecular cloning and expression of the mouse Tnf receptor type b.

A:Reference number: S19021; MUID:92039815

A:Accession: S19021

A:Molecule type: mRNA

A:Residues: 1-454 <ROT>

A:Cross-references: EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849

R:Bebo, B.F. Immunogenetics 39, 450-451, 1994

A:Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cel

A:Reference number: I54532; MUID:94245292

A:Accession: I54532

A>Status: translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-454 <RES>

A:Cross-references: GB:L26349; NID:g430732; PIDN:AAA59361.1; PID:g430733

C:Comment: This protein is one of two distantly related receptors for both TNF-alpha

C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

C:Keywords: duplication; glycoprotein; receptor; transmembrane protein

F:1-29/Domain: signal sequence #status predicted <SIG>

laminin gamma 2 ch
notch4 - mouse
membrane glycoprot
hypothetical prote
T-cell antigen 4-1
hypothetical prote
furin (EC 3.4.21.7
laminin beta-1 cha
latent transformin
VLDL receptor prec
laminin alpha-1 ch
4-IBB - human
lymphocyte activat
gene shuttle craft
laminin beta-1 cha
hypothetical prote

F:30-454/Product: tumor necrosis factor receptor type 1 #status predicted <M>
F:30-212/Domain: extracellular #status predicted <EXT>
F:44-83/Domain: NGF receptor repeat homology <NGL>
F:44-83/Domain: NGF receptor repeat homology <NGL>
F:44-126/Domain: NGF receptor repeat homology <NG3>
F:127-167/Domain: NGF receptor repeat homology <NG3>
F:168-204/Domain: NGF receptor repeat homology <NG4>
F:213-235/Domain: transmembrane #status predicted <MEM>
F:236-454/Domain: intracellular status predicted <INT>
F:54-151-202/Binding site: carbohydurate (Asn) (covalent) #status predicted

Query Match 7.0%; Score 157; DB 1; Length 454;
Best Local Similarity 21.0%; Pred. NO. 0.00018;
Matches 76; Conservative 42; Mismatches 140; Indels 104; Gaps 19;

[illegible]

RESULT 2
157826
tumor necrosis factor receptor - mouse
C:Species: Mus musculus (house mouse)
C:date: 02-Aug-1996 #sequence revision 02-Aug-1996 #text change 23-Jul-1999

R;Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.
Mol. Immunol. 30, 165-176, 1993

A:Title: Genomic organization and promoter function of the murine tumor necrosis factor

A:Reference number: I57826; MUID:93156721

A:Accession: I57826

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-454 <RES>

A:Cross-references: GB:M76656; NID:g202100; PIDN:AAA40465.1; PID:g202102

C:Genetics:

A:Gene: TNFR-2

A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1

C:Superfamily: tumor necrosis

C:Keywords: cytokine receptor

F:44-82/Domain: NGF receptor

F:repeat homology <NGF>

```

Query Match          7.0%; Score 157; DB 2; Length 454;
Best Local Similarity 21.0%; Pred. No. 0.00018;
Matches 76: Conservative 42; Mismatches 140; Indels 104; Gaps 19;

```

QY 34 CROEFRDRSGNCVPCNQCGPMELSKECGFGYGEDAQCVCRLHRRKEDWGF-QKCKPC 92

Db	44	CPQCKYVHSHNNISCTCKCHKHTYLLVSDCP-SPGRDTVCRECEBKGTFTTASQNYLROCLSC	102
Qy	93	LDC-AVYNRFQKANCATSDAICG-----DCLPGFYRKTKL-----	127
Db	103	KTCRKENSQVEIISPCQADKDTVCCKENOFORYLSETHFOCVDCSPFCNGTVTIPCKETQ	162
Qy	128	-----VGF--QDMCEVPCGPPPPYEPHCASKYNLVKIA-----STASSPRDTHAANV	173
Db	163	NTVCNCHAGFFLRESECVPCS-----HCKKNEECMKLCLPPLANVTNPQDSGTAVL	214
Qy	174	ICSAIATVLLALLILCVYICKRFQFMEKKPSWSLRSODIQYNGSELSCLDROPQLHVEYAHRA	233
Db	215	L-----PLVILGLCLLSFT--SLMCRYPRM-----RPEVYSII-----	248
Qy	234	CCQCRDSV----QTCG-PVRLLPSCCEEACSPNATLCGCVGSHSAASLQARN-----	281
Db	249	---C-RDPVPVKBEKAGKPLTPAPSPAFSTSGFNP-TLGFSTPGSSSPVSTPISPIEG	303
Qy	282	-----AGPAGEXMPTFGS--LTQSIGC-----EFSDAWPLMONPMGGONISFCDSYPPEL	329
Db	304	PSNWHMPPYSEVVPQTQADPLLYESICSVPAITSVQKNWEDSAHPQRPDNADLAILYAVV	363
Qy	330	TG 331	
Db	364	DG 365	

RESULTS

JN0006
nerve growth factor receptor, low affinity precursor - chicken
N:Alternate names: NGF receptor
C:Species: Gallus gallus (Chicken)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JN0006; A60504
R:Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Rader,
Neuron 2, 1123-1134, 1989
A:Title: Structure and developmental expression of the nerve growth factor receptor i
A:Reference number: JN0006; MUID:90166579
A:Accession: JN0006.
A:Molecule type: mRNA
A:Residues: 1-416 <LAR>
A:Experimental source: embryonic chick brain
R:Heuer, J.G.; Fatemi-Nainie, S.; Wheeler, E.F.; Bothwell, M.
Dev. Biol. 137, 287-304, 1990
A:Title: Structure and developmental expression of the chicken NGF receptor.
A:Reference number: A60504; MUID:90152140
A:Accession: A60504

A: Status: preliminary; not compared with conceptual translation

A: Molecule type: mRNA

A: Residues: 21-35,'Y',37-172,'K',174-275,'S',277-395,'R',397-416 <HEU>

C: Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastom

C: Comment: The cysteine-rich region of the extracellular domain may form part or all

C: Comment: This protein is thought to form a high-affinity receptor when it associate

C: Superfamily: nerve growth factor receptor; NGF receptor repeat homology

C: Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor

F: 1-20/Domain: signal sequence #status predicted <SIG>

F: 21-416/Product: nerve growth factor receptor #status predicted <MAT>

F: 21-239/Domain: extracellular #status predicted <EXT>

F: 24-57/Domain: NGF receptor repeat homology <NG1>

F: 59-100/Domain: NGF receptor repeat homology <NG2>

F: 101-139/Domain: NGF receptor repeat homology <NG3>

F: 141-181/Domain: NGF receptor repeat homology <NG4>

F: 189-237/Region: serine/threonine-rich

F: 240-261/Domain: transmembrane #status predicted <MEM>

F: 262-416/Domain: intracellular #status predicted <INT>

F: 52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.5%; Score 147; DB 1; Length 416;
Best Local Similarity 29.9%; Pred. NO. 0.00093;
Matches 56; Conservative 17; Mismatches 82; Indels 32; Gaps 10;

QV 20 LGYLSCKVTCETGD-----CROQEEFDR-SGNCVPCNOCGPGMELSKCEGFGY-----G 67

Db 82 VGLHMSAPVESDDAVRCAYGYFQDELSGSKCEKIC-----EVGFLMPFPCRD 133
Qy 68 EDAQCVCRLHREFKDWGKCKPCLDCAVV--NRFQKANGSATSADCGDLPGFYRKT 125
Db 134 QTVCEECPEGTFSDEANF--VDPCLPTICEENVMVKECTASDAECRDLHPRTWHT 191
Qy 126 -KLGVFODMECVPCDPPPPYEPHCASKVNLVKTASTASSP---RDTA--LAAVICSALA 179
Db 192 PSLAGSDSPE--PITRDFPNTGEMATTIADIVTTVMGSSQPVWSRGTDNLIPVYCSILA 249
Qy 180 TVLLALL 186
Db 250 AVVWGLV 256

RESULT 4
A55677
laminin beta-2 chain precursor (version 1) - human
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 17-Mar-1999
C:Accession: A55677
R:Wexler, U.M.; Gerecke, D.R.; Durkin, M.E.; Kurtz, K.S.; Mattei, M.G.; Champliaud, M.F.;
Genomics 24, 243-252, 1994
A:Title: Human beta2 chain of laminin (formerly S chain): cDNA cloning, chromosomal loca
A:Reference number: A55677; MUID:95213013
A:Accession: A55677
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1797 <NEW>
A:Cross-references: GB:X79683
C:Genetics:
A:Gene: GDB:LAMB2
A:Cross-references: GDB:L32363; OMIM:150325
A:Map position: 3p21.3-3p21.2
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C:Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-1797/Product: laminin beta-2 chain #status predicted <MAT>
F:283-344/Domain: laminin-type EGF-like homology <LE01>
F:347-407/Domain: laminin-type EGF-like homology <LE02>
F:410-467/Domain: laminin-type EGF-like homology <LE03>
F:470-519/Domain: laminin-type EGF-like homology <LE04>
F:522-552/Domain: laminin-type EGF-like homology <LE05>
F:783-828/Domain: laminin-type EGF-like homology <LE06>
F:831-874/Domain: laminin-type EGF-like homology <LE07>
F:877-924/Domain: laminin-type EGF-like homology <LE08>
F:927-982/Domain: laminin-type EGF-like homology <LE09>
F:985-1034/Domain: laminin-type EGF-like homology <LE10>
F:1037-1091/Domain: laminin-type EGF-like homology <LE11>
F:1094-1139/Domain: laminin-type EGF-like homology <LE12>
F:1142-1186/Domain: laminin-type EGF-like homology <LE13>

Query Match 6.5%; Score 147; DB 2; Length 1797;
Best Local Similarity 22.4%; Pred. No. 0.0046;
Matches 88; Conservative 35; Mismatches 144; Indels 136; Gaps 24;
Qy 17 LVLLGYLSCKVTCERGDCRQQRDRSGNVC-----PCNQCGPGMSEKCEGFGYG- 67
Db 775 LIYNGALPCQ--CNPQGSLSSECNPHGQCICKPGVVGRRCTCAPY-----YGFGP 825

Qy 68 -----EDAQCVCRLHREF-----KEDWGFQKCKPCL----- 93
Db 826 TGCQACQCSPRGALSSLCERTSGQCL-CRTGAFGLRCDACQRGQWGFPPSCRPCVNGHAD 884
Qy 94 DCVVNRFOKA--NC-SATSDAICGDCLPGFYRKYKLVGFQDMCEVPCGDDPP-PPYEPHC 149
Db 885 EC---NTHTGACLGCRDLTGGHEHCERCITAGFHGDPRLP--YGAQCRPCPCPEGPGQRHF 939
Qy 150 ASKVNVLKVIATSPPTALAAVICSALATVLLALLILCVYCKRFQME-KKP----- 202
Db 940 AT-----SCHQDEYSQOIYCHCRAGY---TGLRCEACAPGQFGDPSRPGACQLC 985

Qy 203 --SWSLRSDIO-----YNGSELSC-----DRPOLHEYA-----HRACQCRRDS 241
Db 986 ECSGNIDPMDPADCPHPGQCQLRCLHTEGPHCAHSKGFHGQAAARQSCHRCTNLLGTN 1045
Qy 242 VQTC-----GPVRLPSM--CCCEACSPN--PATLGGCGVHSAASLAQARNAGP- 284
Db 1046 PQQCPSPDQCHDPSGGQCPCLPNVQALAVDRCAPFNWLTSGHGCQPCACLPSPREGPT 1105
Qy 285 ----AGEMVP--TFRGSLSLTQSGEFSDAWPLMQ 312
Db 1106 CNEFTGQCHPGAGFGGRTCSECOELHWDGDPGLQ 1138

RESULT 5
MURTS
laminin beta-2 chain precursor - rat
N:Alternate names: laminin chain B3; S-laminin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 10-Dec-1999
C:Accession: S03539
R:Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.
Nature 338, 229-234, 1986
A:Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the ne
A:Reference number: S03539; MUID:89159410
A:Accession: S03539
A:Molecule type: mRNA
A:Residues: 1-1801 <HUN>
A:Cross-references: EMBL:X16563; NID:957250; PIDN:CAA34561.1; PID:957251
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type lamin
C:Function:
A:Description: interact with cells and with other basement membrane proteins to promo
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellu
F:1-35/Domain: signal sequence #status predicted <SIG>
F:36-1801/Product: laminin beta-2 chain #status predicted <MAT>
F:36-285/Domain: VI <DOM6>
F:286-555/Domain: V <DOM5>
F:286-347/Domain: laminin-type EGF-like homology <LE01>
F:350-410/Domain: laminin-type EGF-like homology <LE02>
F:413-470/Domain: laminin-type EGF-like homology <LE03>
F:473-522/Domain: laminin-type EGF-like homology <LE04>
F:525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>
F:556-784/Domain: IV <DOM4>
F:786-831/Domain: laminin-type EGF-like homology <LE06>
F:788-1196/Domain: III <DOM3>
F:834-877/Domain: laminin-type EGF-like homology <LE07>
F:880-927/Domain: laminin-type EGF-like homology <LE08>
F:930-986/Domain: laminin-type EGF-like homology <LE09>
F:989-1038/Domain: laminin-type EGF-like homology <LE10>
F:1041-1095/Domain: laminin-type EGF-like homology <LE11>
F:1098-1143/Domain: laminin-type EGF-like homology <LE12>
F:1146-1190/Domain: laminin-type EGF-like homology <LE13>
F:1197-1412/Domain: II <DOM2>
F:1197-1412/Region: heptad repeats
F:1413-1445/Domain: alpha <ALP>
F:1446-1801/Region: heptad repeats
F:1446-1801/Domain: I <DOM1>
F:45-50/Disulfide bonds: #status predicted
F:251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #statu
F:1193,1196,1800/Disulfide bonds: interchain #status predicted

Query Match 6.5%; Score 146.5; DB 1; Length 1801;
Best Local Similarity 22.9%; Pred. No. 0.005;
Matches 99; Conservative 33; Mismatches 146; Indels 155; Gaps 27;
Qy 17 LVLLGYLSCKVTCERGDCRQQRDRSGNVCPCNQCGPMSELSKEC-----GFG--- 65
Db 778 LIYNGALPCQ--CDPQGSLSSECNPHGQC-----RCKPGV-VGRRCDACATGYGFGPAG 830
Qy 66 -----YGEDAQCVTCRLHREF-----KEDWGFQKCKPCLDCAVNRNF 101

Db 831 CQACQSPDGAISALCEGTSGOCL-ORTGAFGLRCDHCQRGOWFPNCRPC-----VCNG 884
 QY 102 QKANCATSDAI-----CGDCLPGFYRKTKL-VGFODMECVPCGDDP-PPYEPH 148
 Db 885 RADECDHTGACGLGCRDYTGGEHCERCIAGFDHPLPYGGQ---CRPCPEGPGSQRH 941
 QY 149 CASKVNLVXIATSPASPRDTALAAVLSALATVLLALLILCVYCKRQFME-KKPSWSLR 207
 Db 942 FAT-----SCHRDGYSQIIVCHCRAGY---TGLRCEACAPGHEGDKSPKPGRCQ 987
 QY 208 -----SDIO-----YNGSELSCLD-----RPQLHEYA-----HRACQOCRR 239
 Db 988 LCSCSGNIDPTDPAACDPHTGQCLRLHTEGPHGCHGCKPGEHGAARQSRCHRTCNLLG 1047
 QY 240 DSVQTC-----GPNVRLLP---SMCCCEACSPN-PATLCGCGVHSAASLAARNA 282
 Db 1048 TDPQPCSTDLCHCDPSTGQCPLPHVQGLSCDR-CAPFNWFTSGRGQCPACHPFSRAR 1106
 QY 283 GP-----AGEMVPTFFGSLTQSGEFSDAWPLMQ-----NPMGGD----- 318
 Db 1107 GPTCNEFTGOCHCHAG-----FGGRTSECQELHWGDFGLQCRACDCDPRGIDKPCQHR 1160
 QY 319 NISFCDSPBELTG 331
 Db 1161 STGHCSGCRPGVSG 1173

RESULT 6
 I54182
 tumor necrosis factor receptor 2-related protein - human
 C:Species: Homo sapiens (man)
 C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
 C:Accession: I54182
 R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
 Genomics 16, 214-218, 1993
 A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen
 A:Reference number: I54182; MUID:93252381
 A:Accession: I54182
 A>Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-435 <RES>
 A:Cross-references: GDB:L04270; NID:G339761; PIDN:AAA36757.1; PID:G339762
 A:Gene: GDB:LTBR
 A:Map position: 12p13.3-12p13.1
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 6.5%; Score 145.5; DB 2; Length 435;
 Best Local Similarity 21.4%; Pred. No. 0.0013;
 Matches 73; Conservative 41; Mismatches 108; Indels 119; Gaps 19;

QY 16 LVLLVLYLSCK-----VTCETGDCRQOB---FRDRSGNVCPCNCGPGMELSKCEGFG 65
 Db 18 VLGLGLLAASQPAVPPVASENQTCDQKEYEYEPQHRIIC--CSRCPPTGVYSARK--S 73
 QY 66 YGEDAQCVTRLHRFRFEDWGF-----QKCRPC-----LDCAVNVRQKANCATSATDAIC- 114
 Db 74 RIRDTVCATCAENSYNHNNYLTICQLCRPCDPVMGLEIAPCTSKRKTQCRQCPGMFCA 133
 QY 115 -----GDCLPGFYRKTK-LVGFDMECVPC-----GDPPEYEPH--CAS 151
 Db 134 AWALECTHCELLSDCPGTEAEKLDKGVGNHNCVCKAGHFQNTSPSARCQPHRTFEN 193
 QY 152 KVNVLVXIA-----STASSPRD-----TALAIVCSALATVLLALLILCVIY---- 192
 Db 194 Q-GLVVEAAPGTAQSDTCKNPLEPLPPEMSGTMLMLAVLLPLAFFLLLATVFCIWKSH 252
 QY 193 --CKR--QFMEKKP-----SNLSRSQDIQYNGSELSCLDRPOLHEYAHRACCOQR 238
 Db 253 SLCKRLGSLKRRQPGEGPNPVAGSW-----EPPKAHPFYF----- 287

QY 239 RDSVQTCGPVRLLPSCMCCEACSPNATLGCQGVHSAASLQA 279
 Db 288 PDLVQPLLP-----SGDVSPVSTGLPAAPVLEA 316

RESULT 7
 SI2783
 OX40 antigen precursor - rat
 N:Alternate names: nerve growth factor receptor homolog
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
 C:Accession: SI2783; S08036
 R:Maillett, S.; Fossum, S.; Barclay, A.N.
 EMBO J. 9, 1063-1068, 1990
 A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphoc
 A:Reference number: SI2783; MUID:90214614
 A:Accession: SI2783
 A:Molecule type: mRNA
 A:Residues: 1-271 <MAL>
 A:Cross-references: EMBL:X17037; NID:G57830; PIDN:CAA34897.1; PID:G57831
 C:Superfamily: CD27 antigen; NGF receptor repeat homology
 C:Keywords: growth factor receptor; transmembrane protein
 F:1-19/Domain: signal sequence #status predicted <Sig>
 F:20-271/Product: OX40 antigen #status predicted <MAT>
 F:211-235/Domain: transmembrane #status predicted <TMM>

Query Match 6.4%; Score 145; DB 2; Length 271;
 Best Local Similarity 28.6%; Pred. No. 0.00083;
 Matches 54; Conservative 23; Mismatches 76; Indels 36; Gaps 12;

QY 9 QEKTFTELLVLLGLYLSCKVTCETGDCRQOEFRRDR--SGN-CVPCNCGPGMELSKCEGFG 65
 Db 6 QQPTAFLLGLSLGVIVKLN-----VKDTYPSGHKC--CRECPQGHGMVSR--D 52
 QY 66 YGEDAQCVTRLHRFRFEDWGFQKCKPCLDCAVVNRQ-KANCATSATDAICGCLCPGFYRK 124
 Db 53 HTRDTVCHPCPCPGFYNEAVNYDTCKQCTQCNHRSGSELKQNTPTEDTVC-QCRPGTQPR 111
 QY 125 TKLVGFQDMCEVPCGDPPEYEP-----HCASKVNLV-----KIATASSPRDTALAIVC- 175
 Db 112 QDSSHLKGLVDCVPC--PPGHFSPGSGNQACKPWTNCTLSKQIRHPASNSLDT-----VCE 164
 QY 176 --SALATVL 182
 Db 165 DRSLLATLL 173

RESULT 8
 I48700
 gene OX40 protein - mouse
 N:Alternate names: OX40 antigen
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
 C:Accession: I48700; I48334; S34377
 R:Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.
 J. Immunol. 151, 5261-5271, 1993
 A:Title: Cloning of mouse OX40: a T cell activation marker that may mediate T-B cell
 A:Reference number: I48700; MUID:94044750
 A:Accession: I48700
 A>Status: translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-272 <RES>
 A:Cross-references: EMBL:Z21674; NID:G312827; PIDN:CAA79772.1; PID:G312828
 R:Birdland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
 Eur. J. Immunol. 25, 926-930, 1995
 A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX
 A:Reference number: I48334; MUID:95255413
 A:Accession: I48334
 A>Status: translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-14, 'G', 16-272 <RE2>
 A:Cross-references: EMBL:X85214; NID:G732818; PIDN:CAA59476.1; PID:G732819

C;Genetics:
A:Gene: 0x40

A:Gene: 0x40

A; Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1

C; Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 6.4%; Score 144; DB 2; Length 272;
Best Local Similarity 29.5%; Pred. No. 0.00099;
Matches 54; Conservative 21; Mismatches 76; Indels 32; Gaps 13;

QY	15	TLVLVLLGYLSCVVCETGDCRQEFDRDSN-CVPNCQCGPMELSKCEGGYGEDAQCV	73
Db	9	TALLLLA-LTLGVTAARLUNCVKHTY--PSGHKC--CRECQPGHGMVSRC--DHTRDTLCH	61
QY	74	TCRLHREFEDGFOKCKPCLDCAVVNRFO--KANCATSDAICGDCCLPGFYRKTCLGVFOD	133
Db	62	PCETGYNEAVNYDFCKCTOCNHRSGSELQNCTPTQTVC-RCRPGQPR-----QD	114
QY	133	-----MECVPCGDPPPPYEP-----HCASKVNVLKVIASTASSPRDTALAAVIC---SALA	175
Db	115	SCYKLGVDVCPC--PPGHFSPGNQACKPWTNCTLSGKOTRIPASDSLDAV-CEDRSLLA	171
QY	180	TVL 182	
Db	172	TLL 174	

RESULT 9

I38869

transcription factor NFX1 [imported] - human

C;Species: Homo sapiens (man)

C:\Program Files\Microsoft Office\Office\Word\Word.exe

C:\Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 02-Sep-2000

C;Accession: I3886

R; Song, Z.; Krishna, S.; Thanos, D.; Strominger, J.L.; Ono, S.J.

J. Exp. Med. 180, 1763-1774, 1994

A;Title: A novel cysteine-rich sequence-specific DNA-binding protein interacts with the

n and functions as a transcriptional repressor.

A;Reference number: I38869; MUID:95053707

A;Accession: I38869

A; Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA
A:Residues: 1-1104 SPEC-

```
A;Residues: 1-1104 <RES>
A:Cross-references: EMPI
```

A;Cross-references: EMBL:U15306; NID:g563216; PIDN:AAA6951/.1; PID:g563217/
C-Superfamily: PING finger homolog

C;superfamily: RING finger homology
F:338-398/Domain: RING finger homology

F, 538-398/DOMAIN: KING LILGER HOMOTOPY <KRN>

Query Match	6.4%	Score 144;	DB 2;	Length 1104;
Best Local Similarity	18.8%	Pred. No. 0.0045;		
Matches 110;	Conservative	59;	Mismatches 181;	Indels 236;
27:	Gaps			

Qy	24	SCKVCTGTGCRROE	FRDRSGNVCVPNQCGPMELSKEGC	-----FGYGEDAQC-----	72
Db	440	SNCLLHPG	-----PCPPCPAFMTKTCCEGRTRHTRVRCGQAVSVHCNSNPC	484	
Qy	73	---VTCRLHREKEDWG	FQCKPCLDCAVNRFOKANCATS	-DAICGDCLPGPYRKTCLV	128
Db	485	ENILNCQHQHAE	LCHGGQCQPCQ	-IILN--QVCYCGSTSRVLVCGTDV-----GKSD	534
Qy	129	FQGDMEC	-----VPGCD	-----PPP	164
Db	535	FGFDFCLTKCGDLK	CGNHTCSQVCHPQPCQCQCPRL	PQLVRCPCPGCQTPLSLLELGSS	594
Qy	165	PRDTALA	V-----IC-SALATVLLALLIC	-----VYICKRQFMEKK-	201
Db	595	SRKTCMDPVP	SCGKVGCKPLPCGSLDP	IHTCEKLCHEGDCGPVSRVTSVISCRC	654
Qy	202	PSWLSRSDI	-----QVNGSELSCLDPRQ	-----LH--EYA	230
Db	655	PCTSLASEDAT	FMCDKRCNKKRLCGRRKHCNEICCVDEKHCPLN	CGRKLRCGLHRCCEPC	714
Qy	231	HRACCO	-CRRDSVQT	-----CGPVRLFLPSMCC	258

```
QY 280 RNA-CPAG-----EMVPT-----FFGSL 296
      |||
      |||
Db 303 SPVFGPSNHNHFPVPPREVPTQGADPLLGLSL 335

RESULT 11
A26431
  nerve growth factor receptor precursor, low affinity - rat
N:Alternate names: NGF receptor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A26431; PH1229
R:Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
Nature 325, 593-597, 1987
A:Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
A:Reference number: A26431; MUID:87115859
A:Accession: A26431
A:Molecule type: mRNA
A:Residues: 1-425 <RAD>
A:Cross-references: GB:X05137; NID:g56755; PIDN:CAA28783.1; PID:g56756
R:Metzels, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.
Gene 121, 247-254, 1992
A:Title: Regulatory elements and transcriptional regulation by testosterone and retinoid
A:Reference number: PH1229; MUID:93077038
A:Accession: PH1229
A:Molecule type: DNA
A:Residues: 1-20 <MET>
A:Cross-references: GB:X61269
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of
C:Comment: This protein is thought to form a high-affinity receptor when it associates
C:Genetics:
A:Introns: 20/3
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-425/Product: nerve growth factor receptor #status predicted <MAT>
F:30-251/Domain: extracellular #status predicted <EXT>
F:33-66/Domain: NGF receptor repeat homology <NG1>
F:68-109/Domain: NGF receptor repeat homology <NG2>
F:110-148/Domain: NGF receptor repeat homology <NG3>
F:150-190/Domain: NGF receptor repeat homology <NG4>
F:198-249/Region: serine/threonine-rich
F:252-273/Domain: transmembrane #status predicted <MEM>
F:274-425/Domain: intracellular #status predicted <INT>
F:61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.2%; Score 140; DB 1; Length 425;
Best Local Similarity 20.8%; Pred. No. 0.0032;
Matches 85; Conservative 52; Mismatches 172; Indels 100; Gaps 20;

QY 16 LLVLLGLYS--CKVTCTGCRQOEFDRSGNCPNQCQPGMELSKGCGFGVGEDAQC 73
      |||
      |||
Db 18 LLILGLVSSGGAKETSTG-----LYTHSGEC--CKACNLGEGVAQPCG---ANQTVCE 66
      |||
      |||
QY 74 TCRHFRKED--NGFOKCKPCLDCAVVNRQKNCATSDAICGDCCLPGYRKTG----- 126
      |||
      |||
Db 67 PCLDNTFSDVVSATPECKPCTBCLGI-QSMSPAPCVAEADAVC-RCAYGYIQDEETGHC 124
      |||
      |||
QY 127 -----LVGFQDMCEVCGDPPPPYEPHCASKVNLVKTASTASSPRDTALAAVIC 175
      |||
      |||
Db 125 ACSVCEVSGSLVFCQDKQNTVCECP---EGTYSDEANHV-----DPCLPCTVC 171
      |||
      |||
QY 176 SALATVLLALLILCVYCKQFNEKRPWSLSRQDQIQYNGSELSDLRDPQLHEFYAHRAC 235
      |||
      |||
Db 172 EDTERQLRE----CTPWADAECIEICRWIPRSTPTPEGSDSTAPSTQEPVPP----- 220
      |||
      |||
QY 236 QCRDRDSVQTGCPVRLPLSMCEACSPNPATLGLCGVHSAASLQARNAGPAGEMVPTFFGS 295
      |||
      |||
Db 221 --EQD-----LVPSTVADWVT-----VMG-----SSQPVTGTNDLIPVCSI 259
      |||
      |||
```

A:Description: Interact with cells and with other basement membrane proteins to promote C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular F:1-21/Domain: signal sequence #status predicted <STG> F:22-1786/Product: laminin beta-1 chain #status predicted <MAT> F:22-270/Domain: VI <DOM6> F:271-540/Domain: V <DOM5> F:271-332/Domain: laminin-type EGF-like homology <LE01> F:335-395/Domain: laminin-type EGF-like homology <LE02> F:398-455/Domain: laminin-type EGF-like homology <LE03> F:458-507/Domain: laminin-type EGF-like homology <LE04> F:510-540/Domain: laminin-type EGF-like homology #status atypical <LE05> F:541-772/Domain: IV <DOM4> F:773-1182/Domain: III <DOM3> F:773-818/Domain: laminin-type EGF-like homology <LE06> F:821-864/Domain: laminin-type EGF-like homology <LE07> F:867-914/Domain: laminin-type EGF-like homology <LE08> F:917-973/Domain: laminin-type EGF-like homology <LE09> F:976-1025/Domain: laminin-type EGF-like homology <LE10> F:1028-1081/Domain: laminin-type EGF-like homology <LE11> F:1084-1129/Domain: laminin-type EGF-like homology <LE12> F:1132-1176/Domain: laminin-type EGF-like homology <LE13> F:1183-1397/Domain: II <DOM2> F:1183-1397/Region: heptad repeats F:1398-1430/Domain: alpha <ALP> F:1431-1786/Region: heptad repeats F:1431-1786/Domain: I <DOM1> F:22/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted F:30-35/Disulfide bonds: #status predicted F:120,356,519,677,1041,1195,1279,1336,1343,1487,1533,1542,1643/Binding site: carbohydrate F:1179,1182,1785/disulfide bonds: interchain #status predicted

Query Match 5.9%; Score 134; DB 1; Length 1786; Best Local Similarity 20.9%; Pred. No. 0.043; Matches 84; Conservative 32; Mismatches 124; Indels 162; Gaps 24;

QY 21 GYLCKVTCETGDCRQEQFRDRSGNCVP-----CNQCGPMGMSKECGFYGED----- 69
DB 779 GSLSSVCDPNEGOCQ-----CRPNVVGRTCNRCAPGT-----FGFGNGCKPC 821
QY 70 -----AQCVTCLRHPRK-----EDWGFKCKPC-----LDCAVNR 100
DB 822 DCHLQGSASFCAIDAITGCFQGIYARQCDRLCPFYMGFPSCQCCNGHALDCTVT- 880
QY 101 FQKANCATSDAI-----CGDCLPGFVKTKLVGFQDMCEVPCGDDPPP-----YEPHCAS 151
DB 881 ---GECLSCQDTTGHNCERCLAGY-GDPIIGSGD-HCRPCPCPDGDSGQFARSCYQ 935
QY 152 KYNLVKIASSTASPRDTALAAVICSALATVLLALLILCVYCKRQFMERKKPSWLSRSQDI 211
DB 936 DPVTLQLACVC---DPGYIGSRCD-----CASGFFGNPDSDFGGSCQPC 976
QY 212 QYN-----GSELSCL-----DRPQLHEYAH-----RAC----- 234
DB 977 QCHHNIDTTPDACDKDTGRCCLKLYHTEDGCHCQGYGYGDALRQDCKVCNVLGTV 1036
QY 235 -----COCRRDSVQ-TCGPVRLPLPSMCEACSPNATL-----GCCVHSAASLQARN 281
DB 1037 KEHNGSDCHCKATGQCSCLP-NVIGQNC--DRCAPNTWQLASGTGCGPCNCNA--AHS 1091
QY 282 AGPAGEMVPTFFGSLTQTSQCFEFSDAWPLMQNPMGSDNISFC 323
DB 1092 FGPS-----CNEFTGQCQCMGP-FGGRTCSEC 1117

RESULT 13
VNHU
von Willebrand factor precursor - human
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C:Accession: A34480; S02377; A37139; S23676; A25298; A25366; S23618; A94060
R:Mancuso, D.J.; Tuley, E.A.; Westfield, L.A.; Worrall, N.K.; Shelton-Inloes, B.B.; Sora

J. Biol. Chem. 264, 19514-19527, 1989
A:Title: Structure of the gene for human von Willebrand factor.
A:Reference number: A34480; MUID:90062044
A:Accession: A34480
A:Molecule type: DNA
A:Residues: 1-2813 <MAN>
A:Cross-references: EMBL:M25864
R:Bonthron, D.; Orkin, S.H.
Eur. J. Biochem. 171, 51-57, 1988
A:Title: The human von Willebrand factor gene. Structure of the 5' region.
A:Reference number: S02377; MUID:88111704
A:Accession: S02377
A:Molecule type: DNA
A:Residues: 1-177 <BO2>
A:Cross-references: EMBL:X06828
R:Mancuso, D.J.; Tuley, E.A.; Westfield, L.A.; Lester-Mancuso, T.L.; Le Beau, M.M.; S
Biochemistry 30, 253-269, 1991
A:Title: Human von Willebrand factor gene and pseudogene: structural analysis and dif
A:Reference number: A37139; MUID:91105089
A:Accession: A37139
A:Molecule type: DNA
A:Residues: 990-1947 <MAD>
A:Cross-references: GB:M60675; NID:g340357; PIDN:AAA61295.1; PID:g553810
A:Note: the authors translated the codon CGC for residue 156 as Gln
R:Collins, C.J.; Underdahl, J.P.; Levene, R.B.; Ravera, C.P.; Morin, M.J.; Dombalagia
Proc. Natl. Acad. Sci. U.S.A. 84, 4393-4397, 1987
A:Title: Molecular cloning of the human gene for von Willebrand factor and identifica
A:Reference number: S23676; MUID:87260814
A:Accession: S23676
A:Molecule type: DNA
A:Residues: 2731-2813 <COL>
A:Cross-references: EMBL:M16945
R:Bonthron, D.; Orr, E.C.; Mitsos, L.M.; Ginsburg, D.; Handin, R.I.; Orkin, S.H.
Nucleic Acids Res. 14, 7125-7127, 1986
A:Title: Nucleotide sequence of pre-pro-von Willebrand factor cDNA.
A:Reference number: A25298; MUID:87016349
A:Accession: A25298
A:Molecule type: mRNA
A:Residues: 1-470, 'V', 472-2813 <BON>
R:Verweij, C.L.; Diergaarde, P.J.; Hart, M.; Pannekoek, H.
EMBO J. 5, 1839-1847, 1986
A:Title: Full-length von Willebrand factor (vWF) cDNA encodes a highly repetitive pro
A:Reference number: A91044; MUID:87004550
A:Accession: A25469
A:Molecule type: mRNA
A:Residues: 1-470, 'V', 472-483, 'R', 485-1022, 'K', 1024-1025, 'E', 1027-1400 <VER>
A:Cross-references: EMBL:X04146
R:Verweij, C.L.; Diergaarde, P.J.; Hart, M.; Pannekoek, H.
EMBO J. 5, 3074, 1986
A:Reference number: A91056
A:Accession: A25366
A:Molecule type: mRNA
A:Residues: 1021-1030 <VE2>
A:Note: this is a revision to the sequence from reference A91044
R:Shelton-Inloes, B.B.; Broze Jr., G.J.; Miletich, J.P.; Sadler, J.E.
Biochem. Biophys. Res. Commun. 144, 657-665, 1987
A:Title: Evolution of human von Willebrand factor: cDNA sequence polymorphisms, repea
A:Reference number: S23618; MUID:87213253
A:Accession: S23618
A:Molecule type: mRNA
A:Residues: 1-120 <SH2>
A:Cross-references: EMBL:M17588; NID:g799330; PIDN:AAA65940.1; PID:g340316
A:Accession: S23645
A:Molecule type: protein
A:Residues: 23-56 <SH3>
R:Sadler, J.E.; Shelton-Inloes, B.B.; Sorace, J.M.; Harlan, J.M.; Titani, K.; Davie,
Proc. Natl. Acad. Sci. U.S.A. 82, 6394-6398, 1985
A:Title: Cloning and characterization of two cDNAs coding for human von Willebrand fa
A:Reference number: A94060; MUID:86016708
A:Accession: A94060
A:Molecule type: mRNA

A:Residues: 'WA',739,'C',744-769,'H',771-788,'A',790-803,'S',805-873;1289-1471,'D',1473-
A:Note: the authors translated the codon TCG for residue 2168 as Cys
R:Shelton-Inloes, B.B.; Titani, K.; Sadler, J.E.
Biochemistry 25, 3164-3171, 1986
A:Title: cDNA sequences for human von Willebrand factor reveal five types of repeated do
A:Reference number: A90504; MUID:86269894
A:Accession: A90504
A:Molecule type: mRNA
A:Residues: 781-788,'A',790-1424 <SHE>
A:Note: 852-Gln, 857-Asp, and 1381-Thr were also found
R:Ginsburg, D.; Handin, R.I.; Bonthron, D.T.; Donlon, T.A.; Bruns, G.A.P.; Latt, S.A.; C
Science 228, 1401-1406, 1985
A:Title: Human von Willebrand factor (vWF): isolation of complementary DNA (cDNA) clones
A:Reference number: A44178; MUID:85244588
A:Accession: A44178
A:Molecule type: mRNA
A:Residues: 2621-2813 <GIN>
A:Cross-references: EMBL:X03028; NID:g340308; PIDN:AAA61293.1; PID:g340309
R:Verweij, C.L.; de Vries, C.J.M.; Distel, B.; van Zonneveld, A.J.; van Kessel, A.G.; v
Nucleic Acids Res. 13, 4699-4717, 1985
A:Title: Construction of cDNA coding for human von Willebrand factor using antibody prob
A:Reference number: S07363; MUID:85269603
A:Accession: S07363
A:Molecule type: mRNA
A:Residues: 2731-2813 <VE3>
A:Cross-references: EMBL:X02672; NID:g37939; PIDN:CAA26503.1; PID:g37940
R:Lynch, D.C.; Zimmerman, T.S.; Collins, C.J.; Brown, M.; Morin, M.J.; Ling, E.H.; Livin
Cell 41, 49-56, 1985
A:Title: Molecular cloning of cDNA for human von Willebrand factor: authentication by a
A:Reference number: S23678; MUID:85201687
A:Accession: S23678
A:Molecule type: mRNA
A:Residues: 2731-2813 <LYN>
A:Cross-references: EMBL:X03028
R:Titani, K.; Kumar, S.; Takio, K.; Ericsson, L.H.; Wade, R.D.; Ashida, K.; Walsh, K.A.;
Biochemistry 25, 3171-3184, 1986
A:Title: Amino acid sequences of human von Willebrand factor.
A:Reference number: A90505; MUID:86269895
A:Accession: A90505
A:Molecule type: protein
A:Residues: 764-788,'A',790-1471,'D',1473-2813 <TIT>
A:Note: 789-thr was also found
R:Chopek, M.W.; Girna, J.P.; Fujikawa, K.; Davie, E.W.; Titani, K.
Biochemistry 25, 3146-3155, 1986
A:Title: Human von Willebrand factor: a multivalent protein composed of identical subuni
A:Reference number: A23464; MUID:86269892
A:Accession: A23464
A:Molecule type: protein
A:Residues: 764-773;2803-2813 <CHO>
R:Dent, J.A.; Berkowitz, S.D.; Ware, J.; Kasper, C.K.; Ruggeri, Z.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6306-6310, 1990
A:Title: Identification of a cleavage site directing the immunochemical detection of mol
A:Reference number: A36013; MUID:90349604
A:Accession: A36013
A:Molecule type: protein
A:Residues: 1606-1617 <DEN>
R:Pay, P.J.; Kawai, Y.; Wagner, D.D.; Ginsburg, D.; Bonthron, D.; Ohlsson-Wilhelm, B.M.;
Science 232, 995-998, 1986
A:Title: Propolypeptide of von Willebrand factor circulates in blood and is identical to
A:Reference number: A60913; MUID:86208144
A:Accession: A60913
A:Molecule type: protein
A:Residues: 576-590 <FAY>
C:Genetics:
A:Gene: GDB:VWF
A:Cross-references: GDB:110125; OMIM:193400
A:Map position: 12p13.3-12p13.2
A:Introns: 19/1; 74/1; 108/2; 178/1; 219/3; 292/1; 333/1; 370/2; 386/1; 431/3; 478/1; 51
5/1; 1724/1; 1771/1; 1819/1; 1874/1; 1888/3; 1948/1; 2021/3; 2086/1; 2200/1; 2266/3; 230
C:Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology; von
C:Keywords: blood coagulation; cell binding; connective tissue; disulfide bond; duplicat
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-763/Product: von Willebrand antigen II #status predicted <NAL>

F:34-386/Domain: type D repeat 1 <DD1>
F:387-745/Domain: type D repeat 2 <DD2>
F:698-700/Region: cell attachment (R-G-D) motif
F:764-2813/Product: von Willebrand factor #status predicted <MA2>
F:784-865/Domain: D' <DDD>
F:788-833,2216-2261/Region: duplication
F:826-853,2400-2515,2544-2662/Region: duplication
F:842-1130,1934-2203/Region: duplication
F:866-1241/Domain: type D repeat 3 <DD3>
F:1275-1443/Domain: von Willebrand factor type A repeat homology <VWA1>
F:1496-1854/Domain: von Willebrand factor type A repeat homology <VWA2>
F:1689-1854/Domain: von Willebrand factor type A repeat homology <VWA3>
F:1947-2295/Domain: type D repeat 4 <DD4>
F:2296-2330/Domain: type B repeat 1 <VB1>
F:2340-2365/Domain: type B repeat 2 <VB2>
F:2375-2399/Domain: type B repeat 3 <VB3>
F:2430-2497/Domain: von Willebrand factor type C repeat homology <VWC1>
F:2507-2509/Region: cell attachment (R-G-D) motif
F:2581-2647/Domain: von Willebrand factor type C repeat homology <VWC2>
F:2871,1231,1515,1574,2223,2290,2357,2400,2546,2585,2790/Binding site: carbohydrate (A
F:1147/Binding site: carbohydrate (Asn) (covalent) #status atypical
F:1248,1255,1256,1468,1477,1487,1679,2298/Binding site: carbohydrate (Thr) (covalent)
F:1263,1486/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 5.9%; Score 133.5; DB 1; Length 2813;
Best Local Similarity 21.4%; Pred. No. 0.078;
Matches 78; Conservative 38; Mismatches 107; Indels 141; Gaps 19;
QY 44 GNCVP---CNQCGPMELSKCEGFGYGEDAQCVTCRLHRFKEDWQKPKCLDCAVNR 100
Db 2246 GSCVPEEACTQC-----IGEDGV-----QHOFLEAW-VPDHPQCOICTCLSG 2286
QY 101 FQKANCSA-----TSDA-ICGDCLPGYRRTKLVGFQDMEC-----VPCGDPPEPEPHCAS 151
Db 2287 -RVNCTTQPCPTAKAPTCLGCEVRLRNADQCCPEYECVCDPVSCLDPP---VPHCR 2342
QY 152 KVNLVIASTASSPRDTALAAVICSALATVLLALLILCVYCKRQFMKPKSWLSRQDI 211
Db 2343 -----GLQPTLTNPG-----CRPNF----- 2358
QY 212 QYNGSELCLDRPOLHEYAHRAHCCQRRDSVQTCGVPRLLPMS-----CCEE---ACSPNP 264
Db 2359 -----TCACRKE-----ECKRVSPSPCPPHR-LPTLRKTQCCDEYECACNCVN 2400
QY 265 ATLGCGVHSAASLQARNAGPAGWPTFFGSLTQSCIGESDAPL----- 310
Db 2401 STVSCPLGYLASTATNDCG-----CTTTCLDPKVCVHRSTIYPVGQFWEEGCDVCTCT 2454
QY 311 -MONPMGGDNISFCDSYP-----ELTGEDIHSLNPELESSTSLDSNSSQ 353
Db 2455 DMEDAVNGLRVAOCSQKPCEDSCRSFGTYVYLHGECCGRCPLSNACEVVTGSPRDSOSSW 2514
QY 354 DLVG 357
Db 2515 KSVG 2518

RESULT 14
A40558
thrombospondin 1 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 20-Aug-1999
R:Accession: A40558; A37905; B42587; S68787
R:Lawler, J.; Duquette, M.; Ferro, P.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.
Genomics 11, 587-600, 1991
A:Title: Characterization of the murine thrombospondin gene.
A:Reference number: A40558; MUID:92128941
A:Accession: A40558
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1170 <LAN>
A:Cross-references: GB:M62449; GB:M62450; GB:M62451; GB:M62452; GB:M62453; GB:M62454;

M62465; GB:M62466; GB:M62467; GB:M62468; GB:M62469; GB:M62470; NID:G511867; PIDN:AAA5061
R:Bornstein, P.; Alf, D.; Devarayalu, S.; Framson, P.; Li, P.
J. Biol. Chem. 265, 16691-16698, 1990
A:Title: Characterization of the mouse thrombospondin gene and evaluation of the role of
A:Reference number: A37905; MUID:90375546
A:Accession: A37905
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-490 <BOR>
A:Cross-references: GB:J05605; GB:J05606; NID:G201991; PIDN:AAA0431.1; PID:G554390
R:Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seidlin, M.F.; Dixit, V.M.
J. Biol. Chem. 267, 3274-3281, 1992
A:Title: Characterization of mouse thrombospondin 2 sequence and expression during cell
A:Reference number: A42587; MUID:92147683
A:Accession: B42587
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1152, 'P', 1154-1170 <LAH>
A:Cross-references: GB:M87276
A:Note: sequence extracted from NCBI backbone (NCBIP:81501)
R:Chen, H.; Aeschlimann, D.; Nowlen, J.; Mosher, D.F.
FEBS Lett. 387, 36-41, 1996
A:Title: Expression and initial characterization of recombinant mouse thrombospondin 1 a
A:Reference number: S68787; MUID:96234006
A:Accession: S68787
A:Molecule type: protein
A:Residues: 19-26, 'X', 28-37 <CHE>
C:Complex: homotrimer, disulfide linked
C:Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; von
C:Keywords: calcium binding; glycoprotein; homotrimer
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-1170/Product: thrombospondin 1 #status predicted <MAT>
F:317-375/Domain: von Willebrand factor type C repeat homology
F:378-429/Domain: thrombospondin type 1 repeat homology <VWC>
F:434-490/Domain: thrombospondin type 1 repeat homology <THR1>
F:491-547/Domain: thrombospondin type 1 repeat homology <THR2>
F:551-586/Domain: thrombospondin type 1 repeat homology <THR3>
F:248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 5.9%; Score 132.5; DB 2; Length 1170;
Best Local Similarity 21.0%; Pred. No. 0.036;
Matches 88; Conservative 39; Mismatches 141; Indels 151; Gaps 25;
Qy 26 KVTCTGCRQOEFDRSGNCPVPCNQCQPG-----MELSKCEGFGY----- 66
Db 350 KVSQPCIMPCSNATVPD--GEC--CPRCWPSDSADGNSFWSEWTSCTATCGNGIQGRS 405
Qy 67 -----GEDAQCVTCRLH-----RFKEDMGFKCKPCLDCA-----VNNRFOKAN-- 105
Db 406 CDSLNNRCEGSSVQRTCHIQCDKRRFKQDGGWHSWSPSSCVTCGDGVITRIRLCNSP 465
Qy 106 -----CSATSDAICGDCPLGPFYRKTKL 127
Db 466 SPQMGKPCGEARTEKACKKDACPINGWGWSPWMDICSVT-----CGG---GVQRRSRL 518
Qy 128 VGFQDMECVPCDPPPPY-EPHCASKVNLVKIATSPASSPRDTALAAVICSALATVLLALL 186
Db 519 -----CNNPTPQGGKDCVDVTENQVCNKQDCPIDCLSNP-CFAGAK----- 561
Qy 187 ILCVITYKRFMEKKPSNLSRSDIQYNGSELSCILDRPOLHE-----YAHRAACQCRD 240
Db 562 --CTSY-----PDGSKWKGACPGYSGNGIQCKDQVDECKEVPDPCFNHNGEHRCKNTD 612
Qy 241 SVQTC--GPVRLLP-----MCCEACSP-NPATLG---CGVHSAASLQARNAGP 284
Db 613 PGYNCLPCPPRFTGSPQFGRGVEHAMANKQCKPRNPTCDGTHDCNKAACNYLGHYSDP 672
Qy 285 --AGEWVPTFGSLTQSGCEPS--DAMPLOMNPMDGNISF-----CDSYPELTGED 333
Db 673 MYRCECKPGYAGN--GIICGEDTDLDGHP--NENLYCVANATYHCKKDKCNPLNPSGQED 728

RESULT 15
A60771
B-cell activation protein CD40 precursor - human
N:Alternate names: B-cell surface antigen Bp50
C:Species: Homo sapiens (man)
C:Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C:Accession: S04460; A60771
R:Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A:Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
A:Reference number: S04460; MUID:89356608
A:Accession: S04460
A:Molecule type: mRNA
A:Residues: 1-277 <STA>
A:Cross-references: EMBL:X60592; NID:G29850; PIDN:CAA43045.1; PID:G29851
R:Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstrom, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-
A:Reference number: A60771; MUID:89093941
A:Accession: A60771
A:Molecule type: protein
A:Residues: 21-50 <BRA>
A:Experimental source: Burkitt lymphoma cell line Raji
C:Genetics:
A:Gene: GDB:CD40
A:Cross-references: GDB:215268; OMIM:109535
A:Map position: 20q12-20q13.2
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane prot
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F:21-193/Domain: extracellular #status predicted <EXT>
F:194-215/Domain: transmembrane #status predicted <TM>
F:216-277/Domain: intracellular #status predicted <CYT>
F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 5.9%; Score 132; DB 2; Length 277;
Best Local Similarity 24.6%; Pred. No. 0.0081;
Matches 52; Conservative 27; Mismatches 78; Indels 54; Gaps 11;
Qy 34 CRQOEFDRSGNCPVPCNQCQGMELSKCEGFGYGEDAQCVTCRLHRFKEDWG-----F 86
Db 26 CREKOYLINS-QC--CSLCQPGQKLVSDC--TEFTETELCPGGESEFLDTNWRNETHCHQH 80
Qy 87 QKCKPCLDCAVNNRFOKANCSATSDAIC-----GDCLPGFYRKTKL 127
Db 81 KYCDPNLGL----RVQQKGTSET-DTICTCEGWHCTSEACESCVLHRSCTSPGFGVKQIA 135
Qy 128 VGFQDMECVPC-----GDPPPPY-----PHCASKVNLVKIAT-----ASSPRDTALAA 172
Db 136 TGVSDTICEPCVPVGFSSVSSAFKCHPWTSCETKDLVVQOAGTNKTDVCCGPDRLRAL 195
Qy 173 VICSALATVLLALLILCVYKRFMEKKPS 203
Db 196 VVIPIIFGLIFAILLVLFVFIKK---VAKKPT 223

Search completed: February 16, 2001, 21:06:39
Job time: 144 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 16, 2001, 21:05:35 ; Search time 19.12 Seconds
(without alignments)
704.322 Million cell updates/sec

Title: US-09-380-276A-4

Perfect score: 2255

Sequence: 1 MALKVLLQEKEFTFTLLVLL.....LDQSGAIHPATQTSLQEA 417

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	157	7.0	454	1 TNRL_MOUSE	P25118 mus musculus
2	147	6.5	416	1 NGFR_CHICK	P18519 gallus gall
3	146.5	6.5	1801	1 LMB2_RAT	P15800 rattus norv
4	145.5	6.5	435	1 TNRC_HUMAN	P36941 homo sapien
5	145	6.4	271	1 OX40_RAT	P15725 rattus norv
6	144	6.4	272	1 OX40_MOUSE	P47741 mus musculus
7	144	6.4	1104	1 NFXL_HUMAN	Q12986 homo sapien
8	141.5	6.3	461	1 TNRL_RAT	P22934 rattus norv
9	140	6.2	425	1 NGFR_RAT	P07174 rattus norv
10	136.5	6.1	1798	1 LMB2_HUMAN	P55268 homo sapien
11	134.5	6.0	415	1 TNRC_MOUSE	P50284 mus musculus
12	134	5.9	1786	1 LMB1_MOUSE	P02469 mus musculus
13	133.5	5.9	1799	1 LMB2_MOUSE	Q61292 mus musculus
14	133.5	5.9	2813	1 VWF_HUMAN	P04275 homo sapien
15	132.5	5.9	1170	1 TSPL_MOUSE	P35441 mus musculus
16	132	5.9	277	1 CD40_HUMAN	P25942 homo sapien
17	129	5.7	326	1 VT2_MYXVL	P29825 myxoma viru
18	128.5	5.7	1170	1 TSPL_HUMAN	P07996 homo sapien
19	127	5.6	4660	1 LRP2_RAT	P98158 rattus norv
20	126.5	5.6	471	1 TNRL_BOVIN	Q19131 bos taurus
21	125.5	5.6	1173	1 TSPL_XENLA	P35448 xenopus lae
22	124.5	5.5	3712	1 LMA_DROME	Q00174 drosophila
23	121	5.4	349	1 VC22_VARV	P34015 variola vir
24	121	5.4	1192	1 LMG2_MOUSE	Q61092 mus musculus
25	121	5.4	1964	1 NTC4_MOUSE	P31695 mus musculus
26	120.5	5.3	965	1 YNC3_YEAST	P33971 saccharomyc
27	120.5	5.3	2813	1 VWF_CANFA	P28295 canis fami
28	120	5.3	256	1 41BB_MOUSE	Q20334 mus musculus
29	119.5	5.3	1193	1 LMG2_HUMAN	Q13753 homo sapien
30	119	5.3	1680	1 FUR2_DROME	P30432 drosophila
31	119	5.3	1785	1 LMB1_HUMAN	P07942 homo sapien
32	118.5	5.3	863	1 LDVR_CHICK	P98165 gallus gall
33	118	5.2	1592	1 SORL1_CHICK	Q98930 g sortilin-

RESULT	1	ALIGNMENTS
TNRL_MOUSE		
ID	TNRL_MOUSE	STANDARD; PRT; 454 AA.
AC	P25118;	
DT	01-MAY-1992 (Rel. 22, Created)	
DT	01-MAY-1992 (Rel. 22, Last sequence update)	
DT	01-OCT-2000 (Rel. 40, Last annotation update)	
DE	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (TNF-RI) (P55).	
DE	(P55).	
GN	TNFRSF1A OR TNFR1 OR TNFR-1.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=91187885; PubMed=1849278;	
RA	Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,	
RA	Wong G.H., Chen E.Y., Goeddel D.V.;	
RT	"Cloning and expression of cDNAs for two distinct murine tumor	
RT	necrosis factor receptors demonstrate one receptor is species	
RT	specific.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=91246168; PubMed=1645445;	
RA	Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,	
RA	Copeland N.G., Jenkins N.A., Smith C.A.;	
RT	"Molecular cloning and expression of the type 1 and type 2 murine	
RT	receptors for tumor necrosis factor.";	
RL	Mol. Cell. Biol. 11:3020-3026(1991).	
RN	[3]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=91285014; PubMed=1647956;	
RA	Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissoneghis A.M.,	
RA	Gray P.W., Feldmann M., Foxwell B.M.J.;	
RT	"Cloning, expression and cross-linking analysis of the murine p55	
RT	tumor necrosis factor receptor.";	
RL	Eur. J. Immunol. 21:1649-1656(1991).	
RN	[4]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=SPLEEN;	
RC	MEDLINE=92039815; PubMed=1657766;	
RA	Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;	
RT	"Molecular cloning and expression of the mouse Tnf receptor type b.";	
RL	Immunogenetics 34:338-340(1991).	
RN	[5]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=94245292; PubMed=8188324;	
RA	Bebo B.F., Linthicum D.S.;	
RT	"Nucleotide sequence of the TNF type I receptor from a mouse	
RT	endothelioma cell line.";	
RL	Immunogenetics 39:450-451(1994).	
RN	[6]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=93156721; PubMed=8381516;	
RA	Rothe J., Bluethmann H., Gentz R., Lesslauer W., Steinmetz M.;	

34	117.5	5.2	3075	1 LMAL_HUMAN	P25391 homo sapien
35	117	5.2	255	1 41BB_HUMAN	Q07011 homo sapien
36	117	5.2	1106	1 STC_DROME	P40798 drosophila
37	116	5.1	417	1 WSL1_HUMAN	Q93038 h wsl-1 pro
38	116	5.1	1790	1 LMB1_DROME	P1046 drosophila
39	114	5.1	327	1 FASA_MOUSE	P25446 mus musculus
40	114	5.1	455	1 TNRL_HUMAN	P19438 homo sapien
41	113.5	5.0	427	1 NGFR_HUMAN	P08138 homo sapien
42	113	5.0	4753	1 LRP_CAEEL	Q04833 caenorhabdi
43	112.5	5.0	3635	1 LMA5_MOUSE	Q61001 mus musculus
44	112	5.0	461	1 TNRL_PIG	P50555 sus scrofa
45	111.5	4.9	1429	1 LI12_CABEL	P14585 caenorhabdi

RT "Genomic organization and promoter function of the murine tumor
 RT necrosis factor receptor beta gene.";

RL Mol. Immunol. 30:165-175(1993).

CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
 CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
 CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).

CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO

CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS

CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY

CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING

CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO

CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX

CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND

CC NF-KAPPA B SIGNALING (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: TYPE 1 MEMBRANE PROTEIN.

CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).

DR EMBL; M60468; AAA39751.1; -

DR EMBL; M59377; AAA40464.1; -

DR EMBL; X59238; CAA41922.1; -

DR EMBL; X57796; CAA40936.1; -

DR EMBL; L26349; AAA59361.1; -

DR EMBL; W76656; AAA40465.1; -

DR EMBL; M88067; AAA40465.1; JOINED.

DR EMBL; M76655; AAA40465.1; JOINED.

DR PIR; A38634; GQMST1.

DR PIR; S16677; S16677.

DR PIR; S19021; S19021.

DR HSP; P19438; LEXT.

DR MGD; MGI:1314884; TNFRSF1A.

DR INTERPRO: IPR000488; -

DR INTERPRO: IPR001368; -

DR PFAM; PF00020; TNFR_c6; 4.

DR PFAM; PF00531; death; 1.

DR PROSITE; PS00652; TNFR_NGFR_1; 3.

DR PROSITE; PS00500; TNFR_NGFR_2; 3.

DR PROSITE; PS50017; DEATH_DOMAIN; 1.

KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.

FT SIGNAL 1 21

FT CHAIN 22 454

FT DOMAIN 22 212

FT TRANSMEM 213 235

FT DOMAIN 236 454

FT REPEAT 43 82

FT REPEAT 83 125

FT REPEAT 126 166

FT REPEAT 167 196

FT DOMAIN 339 349

FT DOMAIN 356 441

FT DISULFID 44 58

FT DISULFID 59 72

FT DISULFID 62 81

FT DISULFID 84 99

FT DISULFID 102 117

FT DISULFID 105 125

FT DISULFID 127 143

FT DISULFID 146 158

FT DISULFID 149 166

FT DISULFID 168 179

FT DISULFID 182 191

FT DISULFID 185 195

FT CARBOHYD 54

FT CARBOHYD 151 151

FT CARBOHYD 202 202

FT CONFLICT 334 334

SQ SEQUENCE 454 AA; 50129 MW; 0710C2E8C32B6D9 CRC64;

Query Match 7.0%; Score 157; DB 1; Length 454;

Best Local Similarity 21.0%; Pred. No. 4.5e-05;

Matches 76; Conservative 42; Mismatches 140; Indels 104; Gaps 19;

QY 34 CRQEFDRSGNCVPCNQCGPMELSKGEGFGYGDAQCQVTCRLHFRKEDWGF-QKCKPC 92

DB 44 CPOGKYVHSHKNSICCTCKCHKGTLYLSDCP-SPGRDVTVCRECKGTFTASQNYLROCLSC 102

QY 93 LDC-AVNVRFQKANCATSATDAICG-----DCLPGFYRKTKL----- 127

DB 103 KTCRKEMSQVEISPCQADKDTVCCKENQFQRYLSETHFQCVCDFNGTVTIPCKETQ 162

QY 128 -----VGF--QDMCEVCPGDPPTPEPHCASKVNLVKIA-----STASSPRDTALAAV 173

DB 163 NTVNCNCHAGFFFLRESGVPCFS-----HCKNECMKLCPLPPPLANVTNPQDSGTAVL 214

QY 174 ICSALATVLLALILLCVYCKRQFMKPKPSWLSRSDIQVNGSELSCLDRLPQLHEYAHRA 233

DB 215 L---PLVILLGLCLLSFIET--SLMCRYPRW-----RPEVYSII--- 248

QY 234 CCOCRRDSV-----QTCG-PVRLLPSCMCBEACSPNATLCCGVHSAASLQARN----- 281

DB 249 ---C-RDPVPVKEEKAGKPLTPAPSPAFSTSGFNF-TLGFSTPGFSSPVSTPISPIFG 303

QY 282 -----AGPAGEVMPTEFGS--LTQSIGC----EFSDAMPLMONGMGNISPCDSVPEL 329

DB 304 PSNWHFMPVSEVVPVTPQAGDPLLYESLCVSPAPTSVQKWEDESAHPORPDNADLILYAVV 363

QY 330 TG 331

DB 364 DG 365

RESULT 2

NGFR_CHICK

ID NGFR_CHICK STANDARD; PRT; 416 AA.

AC P18519;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)

GN NGFR.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN;

RX MEDLINE=90166579; PubMed=2560385;

RA Large T.H., Weskamp G., Helder J.C., Radeke M.J., Misko T.P.,

RA Shooter E.M., Reichardt L.F.;

RT "Structure and developmental expression of the nerve growth factor

RT receptor in the chicken central nervous system.";

RL Neuron 2:1123-1134(1989).

RP [2]

RP SEQUENCE OF 21-416 FROM N.A.

RX MEDLINE=90152140; PubMed=2154393;

RA Heuer J.G., Fatemie-Nainie S., Wheeler E.F., Bothwell M.;

RT "Structure and developmental expression of the chicken NGF receptor.";

RL Dev. Biol. 137:287-304(1990).

CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,

CC NT-3, AND NT-4.

CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE

ID	LMB2_RAT	STANDARD;	PRT;	1801 AA.
AC	P15800;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3).			
GN	LAMB2.			
GN	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
RC	MEDLINE=89159410; PubMed=2922051;			
RA	Hunter D.D., Shah V., Merlie J.P., Sanes J.R.;			
RT	"A laminin-like adhesive protein concentrated in the synaptic cleft			
RT	of the neuromuscular junction.";			
RL	Nature 338:229-234(1989).			
CC	-!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ			
CC	IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF			
CC	CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING			
CC	WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.			
CC	-!- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE			
CC	DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND			
CC	TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE			
CC	COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.			
CC	THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4			
CC	(S-MEROSIN), AND LAMININ-7 (KS-LAMININ).			
CC	-!- SUBCELLULAR LOCATION: EXTRACELLULAR.			
CC	-!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR			
CC	COMPONENT). S-LAMININ IS CONCENTRATED IN THE SYNAPTIC			
CC	CLEFT OF THE NEUROMUSCULAR JUNCTION.			
CC	-!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT			
CC	WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.			
CC	-!- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.			
CC	-!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).			
CC	-!- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.			
CC	-!- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.			
CC	-----			
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CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/)			
CC	or send an email to license@isb-sib.ch .			
CC	-----			
DR	EMBL; X16563; CAA34561.1; -			
DR	PIR; S03539; MMRTS.			
DR	HSSP; P02468; 1KLO.			
DR	INTERPRO; IPR000561; -			
DR	INTERPRO; IPR001886; -			
DR	INTERPRO; IPR002049; -			
DR	PFAM; PF00053; laminin_EGF; 13.			
DR	PFAM; PF00055; laminin_Nterm; 1.			
DR	PRINTS; PR00011; EGF_LAMININ.			
DR	PROSITE; PS00022; EGF_1; 10.			
DR	PROSITE; PS01186; EGF_2; 2.			
DR	PROSITE; PS01248; LAMININ_TYPE_EGF; 12.			
DR	Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;			
KW	Laminin EGF-like domain; Cell adhesion; Repeat; Signal.			
FT	SIGNAL	1	35	
FT	CHAIN	36	1801	
FT	DOMAIN	36	283	
FT	DOMAIN	286	555	
FT				
FT	DOMAIN	286	349	
FT	DOMAIN	350	412	
FT	DOMAIN	413	472	
FT	DOMAIN	473	524	
FT	DOMAIN	525	555	
FT	DOMAIN	556	785	
FT	DOMAIN	786	1192	
FT				
FT	CHAIN	36	1801	
FT	DOMAIN	36	283	
FT	DOMAIN	286	555	
FT				
FT	DOMAIN	286	349	
FT	DOMAIN	350	412	
FT	DOMAIN	413	472	
FT	DOMAIN	473	524	
FT	DOMAIN	525	555	
FT	DOMAIN	556	785	
FT	DOMAIN	786	1192	
FT				
FT	CHAIN	36	1801	
FT	DOMAIN	36	283	
FT	DOMAIN	286	555	
FT				
FT	DOMAIN	286	349	
FT	DOMAIN	350	412	
FT	DOMAIN	413	472	
FT	DOMAIN	473	524	
FT	DOMAIN	525	555	
FT	DOMAIN	556	785	
FT	DOMAIN	786	1192	
FT				
FT	CHAIN	36	1801	
FT	DOMAIN	36	283	

FT DOMAIN 786 833
 FT DOMAIN 834 879
 FT DOMAIN 880 929
 FT DOMAIN 930 988
 FT DOMAIN 989 1040
 FT DOMAIN 1041 1097
 FT DOMAIN 1098 1145
 FT DOMAIN 1146 1192
 FT DOMAIN 1193 1412
 FT DOMAIN 1413 1445
 FT DOMAIN 1446 1801
 FT DOMAIN 1259 1306
 FT DOMAIN 1475 1529
 FT DOMAIN 1576 1793
 FT DISULFID 286 295
 FT DISULFID 288 313
 FT DISULFID 315 324
 FT DISULFID 327 347
 FT DISULFID 350 359
 FT DISULFID 352 377
 FT DISULFID 380 389
 FT DISULFID 392 410
 FT DISULFID 413 426
 FT DISULFID 415 441
 FT DISULFID 443 452
 FT DISULFID 455 470
 FT DISULFID 473 487
 FT DISULFID 475 494
 FT DISULFID 496 505
 FT DISULFID 508 522
 FT DISULFID 786 798
 FT DISULFID 788 805
 FT DISULFID 807 816
 FT DISULFID 819 831
 FT DISULFID 834 846
 FT DISULFID 836 853
 FT DISULFID 855 864
 FT DISULFID 867 877
 FT DISULFID 880 889
 FT DISULFID 882 896
 FT DISULFID 899 908
 FT DISULFID 911 927
 FT DISULFID 930 946
 FT DISULFID 932 957
 FT DISULFID 959 968
 FT DISULFID 971 986
 FT DISULFID 989 1003
 FT DISULFID 991 1010
 FT DISULFID 1013 1022
 FT DISULFID 1025 1038
 FT DISULFID 1098 1110
 FT DISULFID 1100 1117
 FT DISULFID 1119 1128
 FT DISULFID 1131 1143
 FT DISULFID 1146 1158
 FT DISULFID 1148 1165
 FT DISULFID 1167 1176
 FT DISULFID 1179 1190
 FT DISULFID 1193 1193
 FT DISULFID 1196 1196
 FT DISULFID 1800 1800
 FT CARBOHYD 251 251
 FT CARBOHYD 371 371
 FT CARBOHYD 1088 1088
 FT CARBOHYD 1252 1252
 FT CARBOHYD 1311 1311
 FT CARBOHYD 1351 1351
 FT CARBOHYD 1502 1502
 FT SEQUENCE 1801 AA; 196473 MW; 97AEF32F8F31FA75 CRC64;

Query Match

6.5%; Score 146.5; DB 1; Length 1801;

Best Local Similarity 22.9%; Pred. No. 0.0014;
 Matches 99; Conservative 33; Mismatches 146; Indels 155; Gaps 27;
 QY 17 LVLLGYLSKVCYTCETGDCRQOQEFDRSGNVCVPCNQCQPGMELSKEC-----GFG--- 65
 DB 778 LVYNGALPCQ--CDQGSLSSECNPHGGQC-----RCKPGV-VGRRCDACATGYGFGPAG 830
 QY 66 -----YGEDAQOQCTCLHRF-----KEDMGFKCKPCLDCAVVNR 101
 DB 831 COACQSPDGALSALCEGTSGQL-CRTGAFGLRCDHCQGWGFFNCRPC-----VCNG 884
 QY 102 QKANCATSDAI-----CGDCLPGFYRKTKL-VGFDMECVPCGDDP-PPYEPH 148
 DB 885 RADECDHAHTGACGLGRDYTGGEHCERCIAAGHGDPLRPGYGQ---CRPCPCPEGPGSQRH 941
 QY 149 CASKVNLVKIATSTASSPRDTALAATVCSALATVLLALLILCVIYCKRQME-KKPSWSLR 207
 DB 942 FAT-----SCHRDGYSQOIYVCHCRAGY---TGLRCEACAFGHGDPKPGGRCQ 987
 QY 208 -----SQDIQ-----YNGSELSCLD-----RPLHEYA-----HRACQCR 239
 DB 988 LCECSGNIDPTDPCADPHGTGQCLRLHHTGPHGCHGCRPGHQAARQSCHRCTCNLLG 1047
 QY 240 DSVQTC-----GPVRLLP---SMCCEACSPN--PATLGGCVHSAASLOARNA 282
 DB 1048 TDPQRCPSDLCCHCDPSTGQCPCPLPHVQGLSCDR-CAPNFWNFTSGRCQCPACHPSSAR 1106
 QY 283 GP-----AGENVPTFFGSLTQICGFSFSAWPLMQ-----NPMGCD----- 318
 DB 1107 GPTCNFTGQCHAG-----FGGRTCSQCQLHWGDFGLQCRACDCDPRGIDKPCQCHR 1160
 QY 319 NISFCDSYPELTG 331
 DB 1161 STGHCSCRPGVSG 1173
 RESULT 4
 ID TNRC_HUMAN STANDARD; PRT; 435 AA.
 AC P36941;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
 GN LTBR OR TNFR OR TNFRSF3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=93252381; PubMed=8486360;
 RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
 RT "Construction and evaluation of a hncDNA library of human 12p
 transcribed sequences derived from a somatic cell hybrid.";
 RN Genomics 16:214-218(1993).
 RL [2]
 RP FUNCTION.
 RX MEDLINE=94225209; PubMed=8171323;
 RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
 RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
 RT "A lymphotoxin-beta-specific receptor";
 RN Science 264:707-710(1994).
 CC -!- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
 IMMUNE DEVELOPMENT.
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -----
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CC EMBL; L04270; AAA36757.1; -.
CC HSSP; P25942; ICDF.
CC MIN; 600979; -.
DR INTERPRO; IPR001368; -.
DR PFAM; PF00020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 435
FT DOMAIN 31 227
FT TRANSMEM 228 248
FT DOMAIN 249 435
FT DOMAIN 42 211
FT REPEAT 42 81
FT REPEAT 82 124
FT REPEAT 125 168
FT REPEAT 169 211
FT DISULFID 43 58
FT DISULFID 59 72
FT DISULFID 62 80
FT DISULFID 83 98
FT DISULFID 101 116
FT DISULFID 104 124
FT DISULFID 126 132
FT DISULFID 139 148
FT DISULFID 142 167
FT DISULFID 170 185
FT CARBOHYD 40 40
FT CARBOHYD 177 177
SQ SEQUENCE 435 AA; 46709 MW; 6242626E6022F656F CRC64;

Query Match 6.5%; Score 145.5; DB 1; Length 435;
Best Local Similarity 21.4%; Pred. No. 0.00034;
Matches 73; Conservative 41; Mismatches 108; Indels 119; Gaps 19;

QY 16 LLVLLGYLSCK-----VTCTGDCROE---FDRSGNVCVPCNOCGMELSKCEGFG 65
Db 18 VLGLGLLAASQOAPVYPYASENCTCRDQKEYVEQHRIC--CSRCPGTYVSAKC--S 73

QY 66 YGEDAQCVTCRLHRRFKEDWGF---QKCKPC-----LDCAVNRFOKANGSATSDAIC- 114
Db 74 RIOTVGCATCAENSYNEHWNLTICQLCRPCDPVYMGLEEIAPCTSKRTQCRQCPGMFCA 133

QY 115 -----GDCLPGFYRKTK-LVGFQDMCVPC-----GDPPPPYEPH--CAS 151
Db 134 AWALECTHCELLSDCPGCTEAEKDEVGKGNHCVCKAGHFQNTSSPSARCQPHPTRCEN 193

QY 152 KVNVLKIA-----STASSPRD-----TALAANVCISALATVLLALLILCVIY---- 192
Db 194 Q-GLVEAAPGTAQSDTTCKNLEPLPPMESTGMLMLVLLPLAFLLLATVFCIWKSHGP 252

QY 193 --CKR--QFMKKKP-----SWLSRSDIQYNGSELSCDRPOLHEVAHRAHCCQCR 238
Db 253 SLCKRLGSLKRRQGGEGPNVAGSW-----EPPKAHPF----- 287

QY 239 RDSVQTCGVRLLPSMCCMEACSPNPATLGGCGVHSAASLQA 279
Db 288 PDLVQPLLEPI-----SGDVSPVSTGLPAAPVLEA 316

RESULT 5
OX40_RAT
ID OX40_RAT STANDARD; PRT; 271 AA.
AC P15725;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
```

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DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).
GN TNFRSF4 OR TXGPIL OR OX40.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-CCELL;
RX MEDLINE=90214614; PubMed=2157591;
RA Mallett S., Fossum S., Barclay A.N.;
RT "Characterization of the MRC OX40 antigen of activated CD4 positive T
RL Lymphocytes -- a molecule related to nerve growth factor receptor.";
CC -!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
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EMBL; X17037; CAA34897.1; -.
PIR; S08036; S08036.
PIR; S12783; S12783.
DR HSSP; P25942; ICDF.
DR INTERPRO; IPR001368; -.
DR PFAM; PF00020; TNFR_C6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KW Signal.
FT SIGNAL 1 19
FT CHAIN 20 271
FT DOMAIN 20 210
FT TRANSMEM 211 235
FT DOMAIN 236 271
FT DOMAIN 25 164
FT REPEAT 25 60
FT REPEAT 61 102
FT REPEAT 103 123
FT REPEAT 124 164
FT CARBOHYD 143 143
SQ SEQUENCE 271 AA; 29895 MW; C06465136B16E821 CRC64;

Query Match 6.4%; Score 145; DB 1; Length 271;
Best Local Similarity 28.6%; Pred. No. 0.00022;
Matches 54; Conservative 23; Mismatches 76; Indels 36; Gaps 12;
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QY 9 QEKFTFTLLVLLGYLSCKVTCTGDCROEPRDR--SGN-CVPCNOCGMELSKCEGFG 65
Db 6 QOQTAFLLLGLSLGVTVKLNC-----VKDTPSGHKC--CRECQPHGMVSR--D 52

QY 66 YGEDAQCVTCRLHRRFKEDWGFQKCKPCLDCAVNRFO-KANGSATSDAICDCLPGFYRK 124
Db 53 HTRDTVCHPCBEGFYNEAVNYDTCKQTCQCNHRSSELKQNTPTPTEDIVC-OCRPGTQPR 111

QY 125 TKLVGFQDMCVPCGDPPPPYEP-----HCASKVNIV-----KIATPASSPROTALAIVC- 175
Db 112 QDSSHKLGVDCVPC--PPGHFSPGNSQACKPWTNCTLSKQIRHPASNSLDT-----VCE 164

QY 176 --SALATVL 182
Db 165 DRSLIATLL 173
```

RESULT 6
OX40_MOUSE

ID OX40_MOUSE STANDARD; PRT; 272 AA.
AC P47741;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).
GN TNFRSF4 OR TXGP1 OR OX40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE=94044750; PubMed=8228223;
RA Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J.,
RA Claassen E., Noelle R.J., Feli H.,
RT "Cloning of mouse OX40; a T cell activation marker that may mediate
T-B cell interactions";
RL J. Immunol. 151:5261-5271(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95255413; PubMed=7737295;
RA Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Barclay A.N.;
RT "Gene structure and chromosomal localization of the mouse homologue
of rat OX40 protein";
RL Eur. J. Immunol. 25:926-930(1995).
CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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CC
CC EMBL: Z21674; CAA79772.1; -;
CC EMBL: X85214; CAA59476.1; -;
CC HSP: P25942; ICDP.
DR MGD; MGI:104512; TXGP1.
DR INTERPRO: IPR001368; -;
DR PFAM: PF00020; TNFR_C6; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KW Signal.
FT SIGNAL 1 19 . POTENTIAL.
FT CHAIN 20 272 OX40L RECEPTOR.
FT DOMAIN 20 211 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 212 236 POTENTIAL.
FT DOMAIN 237 272 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 165 4 X TNFR-CYS.
FT REPEAT 26 61 TNFR-CYS 1.
FT REPEAT 62 103 TNFR-CYS 2.
FT REPEAT 104 124 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 125 165 TNFR-CYS 4.
FT CARBOHYD 144 144 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 15 15 A -> G (IN REF. 2).
SQ SEQUENCE 272 AA; 30153 MW; 06E7B84156F0D08E CRC64;

Query Match 6.4%; Score 144; DB 1; Length 272;
Best Local Similarity 29.5%; Pred. No. 0.00026;
Matches 54; Conservative 21; Mismatches 76; Indels 32; Gaps 13;

QY 15 TLVLVLGLYSCKVTCTGCRQEFRRDSGN-CVPCNQCQPGMELSKCEGFGYGEDAQCV 73
DB 9 TALLLLA-LTLGVTRRLNCVKHTY--PSGHKC--CRECPQGHGMYSRC--DHTRTDLCH 61
QY 74 TCRHLRFKEDMGFKCKPCLDCAVNRFO-KANCATSDAICGDCPLPGFYRKTGLGVFQD 132

Db 62 PCETGFYNEAVNYDTCQCTQCNRHSGSELKQNCPTQDTVC-RCRPGTQPR-----QD 114
QY 133 -----MECVPCGDDPPPPYEP-----HCASKVNLVLIASSTASSPRDTALAANVIC-----SALA 179
Db 115 SCYKLGVDVCPC--PPGHFSPGNQACKPWTNCTLSGKQTRHPASDSLDV-CEDRSLLA 171
QY 180 TVL 182
Db 172 TLL 174
RESULT 7
ID NF1L_HUMAN STANDARD; PRT; 1104 AA.
AC Q12986;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE TRANSCRIPTIONAL REPRESSOR NF-X1.
GN NF1L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95053707; PubMed=7964459;
RA Song Z., Krishna S., Thanos D., Strominger J.L., Ono S.J.;
RT "A novel cysteine-rich sequence-specific DNA-binding protein
interacts with the conserved X-box motif of the human major
histocompatibility complex class II genes via a repeated Cys-His
domain and functions as a transcriptional repressor";
RL J. Exp. Med. 180:1763-1774(1994).
CC -1- FUNCTION: REPRESSOR OF HLA-DRA TRANSCRIPTION. BINDS TO THE X-BOX
CC MOTIF OF CLASS II MHC GENES. MAY PLAY AN IMPORTANT ROLE IN
CC REGULATING THE DURATION OF AN INFLAMMATORY RESPONSE BY LIMITING
CC THE PERIOD IN WHICH CLASS II MHC MOLECULES ARE INDUCED BY
CC INTERFERON-GAMMA.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- INDUCTION: BY INTERFERON-GAMMA.
CC -1- SIMILARITY: TO D.MELANOGASTER SHUTTLE CRAFT PROTEIN (STC) AND
CC YEAST YNL023C.
CC
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CC
CC EMBL: U15306; AAA69517.1; -;
CC HSP: P02876; 2WGC.
DR INTERPRO: IPR000967; -;
DR INTERPRO: IPR001374; -;
DR PFAM: PF01424; R3H; 1.
DR PFAM: PF01422; zf-NF-X1; 8.
KW Transcription regulation; Repressor; DNA-binding; Nuclear protein;
KW Repeat.
FT DOMAIN 424 876 7 X APPROXIMATE REPEATS, CYS-RICH.
FT REPEAT 424 463 1.
FT REPEAT 480 517 2.
FT REPEAT 541 580 3.
FT REPEAT 606 647 4.
FT REPEAT 695 734 5.
FT REPEAT 806 842 6.
FT REPEAT 836 876 7.
SQ SEQUENCE 1104 AA; 123149 MW; 36FEC4292F78130C CRC64;

Query Match 6.4%; Score 144; DB 1; Length 1104;
Best Local Similarity 18.8%; Pred. No. 0.0012;
Matches 110; Conservative 59; Mismatches 181; Indels 236; Gaps 27;

QY 24 SKVTCETGDCRQEFDRSGNVCNOCGPGMELSKGCG-----FYGEDAQC----- 72
 DB 440 SCNLLCHPG-----PCPPCPAFMTKTCGGRTRHVRGQAVSVHCNPPC 484
 QY 73 ----VTCRLHRPKEDGFKCKPCLDCAVVRKQKANCATS--DATCGDCLPGFYRKTLV 128
 DB 485 ENILNCGHQCAELCHGGQCPQ---IILN--QVCYCGSTRDVLGGTDV-----GRSD 534
 QY 129 GQDMEC-----VPCGD-----PPP-----PYEHC--ASKVNLVKIATASS 164
 DB 535 GFGDFSLCTCKDLKGNHTCSQVCHQPCQCPRLPOLVRCPCGQPLSOLLELSS 594
 QY 165 PRDTALA--IC-SALATVLLALLILC-----VIYKRRQFMERK- 201
 DB 595 SRKTCMDPVPSCGKGRPLCGSLDFHTCEKLCHEGDCGVPVSRVTSVISCRCSPFREL 654
 QY 202 PWSLRSQDI-----QYNGSELSCLDLRFQ-----LH---EYA 230
 DB 655 PCTLSKSEDATPMCKRCKNKLGRHKNEICCVDKHKPLNCGRLRCGLHRCEPC 714
 QY 231 HRACQ-CRRDSVQT-----CGVRLPLSMCC-----EE 258
 DB 715 HRGNCOTQWASFDELTCGASVYPPVPCGTRPCTQTCARVHECDHPVYHSGHSEE 774
 QY 259 ACS-----PNPATLGGVHSAASL----- 277
 DB 775 KPCCPCTFLTQKCMGKHEFRSNIPCHLVDISGLPCSATLPCGMKHCQRLCHKGLVDE 834
 QY 278 -----QAR-----NAGPAGEMVPTFFGSLTQSI 300
 DB 835 PKQPCTTTPRADCGHPCMAPCHTSPCPVTACKAKVELQCEGRRKEMVICSEASTYQR 894
 QY 301 CEEFSDAWPLMNPMDGNISFCDSPELTGDIDHSLNPELESSTSLDSSQDLVGAV 360
 DB 895 IAAISWASKITDNLGGS-----VEISKLTIKKEVQARLECEDECSALERKAR--LAFAF 948
 QY 361 PVQSHSENFAATDLSRYNNTLIVESASTQDALTMRSQLDQESGAI 406
 DB 949 HISEDSPFNIRSSGSKFSKSLKEDA--RKDLKFVSDVEKEMETLV 992

RESULT 8
 TNRI_RAT
 ID TNRI_RAT STANDARD: PRT: 461 AA.
 AC P22934:
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1992 (Rel. 21, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (TNF-RI) (P35).
 GN TNFRSF1A OR TNFR1 OR TNFR-1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP MEDLINE=91090841; PubMed=1702293;
 RA Himmeler A., Maurer-Poggy I., Kroenke M., Scheurich P., Pfizenmaier K.,
 RA Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
 RT "Molecular cloning and expression of human and rat tumor necrosis
 RT factor receptor chain (p60) and its soluble derivative, tumor
 RT necrosis factor-binding protein.";
 RL DNA Cell Biol. 9:705-715(1990).
 CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
 CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
 CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
 CC -!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY

CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC
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 CC
 CC EMBL; M63122; AAA42256.1; -
 CC PIR; B36555; B36555.
 CC HSP; P19438; ITNR.
 CC INTERPRO: IPR000488; -
 CC INTERPRO: IPR001368; -
 CC PFAM; PF00020; TNFR_C6; 4.
 CC PFAM; PF00531; Death; 1.
 CC PROSITE; PS00652; TNFR_NGFR_1; 3.
 CC PROSITE; PS00650; TNFR_NGFR_2; 3.
 CC PROSITE; PS0017; DEATH_DOMAIN; 1.
 CC Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
 CC SIGNAL 1 21
 FT CHAIN 22 461
 FT DOMAIN 22 211
 FT TRANSMEM 212 234
 FT DOMAIN 235 461
 FT DOMAIN 43 196
 FT REPEAT 43 82
 FT REPEAT 83 125
 FT REPEAT 126 166
 FT REPEAT 167 196
 FT DOMAIN 344 354
 FT DOMAIN 363 448
 FT DISULFID 44 58
 FT DISULFID 59 72
 FT DISULFID 62 81
 FT DISULFID 84 99
 FT DISULFID 102 117
 FT DISULFID 105 125
 FT DISULFID 127 143
 FT DISULFID 146 158
 FT DISULFID 149 166
 FT DISULFID 168 179
 FT DISULFID 182 191
 FT DISULFID 185 195
 FT CARBOHYD 54 54
 FT CARBOHYD 151 151
 FT CARBOHYD 201 201
 SQ SEQUENCE 461 AA; 50969 MW; EB23C05450FBD202 CRC64;
 Query Match 6.3%; Score 141.5; DB 1; Length 461;
 Best Local Similarity 21.6%; Pred. No. 0.00073;
 Matches 72; Conservative 37; Mismatches 113; Indels 111; Gaps 20;
 QY 34 CRQEFDRSGNVCNOCGPGMELSKGCGFYGEDAQCVCRLHRFKEDGFKCKPCL 93
 DB 44 CPGKYAHPKNNISICTCKHKTLYLVSDCP-SFGQETVCEVCDKGTFTASQ--NHVRQL 100
 QY 94 DCAVYNR--FQK--ANCSATSDAICDCLPGFYRKTKLVGFDMECVPC----- 138
 DB 101 SCKTCKEMFQVEISPCADMDTVCGCKKNQFORVLSLTHFQCVDCSPCFNGVTVTIPCKE 160
 QY 139 -----GDDPPPYEPHCASKVNLVKI-----ASTASSPRDTALAATCSALA 179
 DB 161 KONTVCNCHAGFFLSGNETPCS-HCKKNQECMKLCLPPVANVTNPQDSTAVLLPLVIF 219


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FT CARBOHYD 1249 1249 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1308 1308 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1348 1348 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 1499 1499 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 914 914 R -> G (IN REF. 2).
FT CONFLICT 1179 1179 G -> A (IN REF. 2).
SQ SEQUENCE 1798 AA; 196079 MW; 9555CF5B24850CB7 CRC64;

Query Match
Best Local Similarity 6.1%; Score 136.5; DB 1; Length 1798;
Matches 87; Conservative 39; Mismatches 136; Indels 167; Gaps 25;

QY 17 LVLLGYLSKVTGETGDCRQOEFRDSNGCV-----PCNQCGPMELSKCEGFGY- 67
D 17 LVLLGYLSKVTGETGDCRQOEFRDSNGCV-----PCNQCGPMELSKCEGFGY- 67
D 775 LIYNGALPCQ--CNPOGSLSECNPHGGQCLCKPGVVGRCDCLCAPGY-----YGF 825
QY 68 -----EDAQVTCRLHFR-----KEDWGFQCKPCPLDCAVVN 99
D 68 -----EDAQVTCRLHFR-----KEDWGFQCKPCPLDCAVVN 99
D 826 TGCAQACQCSHEGALSICKETSQCL-CRTGAFGLRCDCRQCGWGFPPSCRPCV----- 878
QY 100 RFQKANCATSDAI-----CGDCLPGFYRKTCL-VGFQDMCEVPCGD 140
D 100 RFQKANCATSDAI-----CGDCLPGFYRKTCL-VGFQDMCEVPCGD 140
D 879 -----CNGHADSCNHTGACLRDHTGHEHCERCIAGHRDPLPYGGQ---CRPCPC 929
QY 141 PP-PYPPEPHCASKVNLVKIATASPRDTALAAGVGSALATVLLALLILCVYCKRQFME 199
D 141 PP-PYPPEPHCASKVNLVKIATASPRDTALAAGVGSALATVLLALLILCVYCKRQFME 199
D 930 PEGSGORHPAT-----SCHQDEYSQIVCHCRAGY---TGLRCEACAPGHFGD 975
QY 200 -KKP-----SWSLRSDIO-----YNGSELSCLD-----RPLHBYA----- 230
D 200 -KKP-----SWSLRSDIO-----YNGSELSCLD-----RPLHBYA----- 230
D 976 PSRPGRCQLCEGSGNIDPMDACDPHTGQCLRLHTEGPHCAKCPGFHQAARQSC 1035
QY 231 HRACCOCRRDSVOTC-----GPVRLLPSPM---CCEEACSPN---PATLGGCGVHS 273
D 231 HRACCOCRRDSVOTC-----GPVRLLPSPM---CCEEACSPN---PATLGGCGVHS 273
D 1036 HRTCNLLGTNPQCCSPDOCHDPSGQCPCLPNVGGPSCDR-CAPNFNWLTSGHGCP 1094
QY 274 AASLQARNAGPAGEMVPTFFGSLTQICGFSFSDAWPLMQNPMGDNISFCDSYPELTGED 333
D 274 AASLQARNAGPAGEMVPTFFGSLTQICGFSFSDAWPLMQNPMGDNISFCDSYPELTGED 333
D 1095 CACHPSRARGPT-----CNEFTGOCHCRAG-FGGRTCSEC-----QE 1130
QY 334 IHSNLEPE 342
D 334 IHSNLEPE 342
D 1131 LHWGDFGLQ 1139

RESULT 11
TNRC_MOUSE STANDARD; PRT; 415 AA.
AC P50284;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
GN LTBR OR TNFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CVB; TISSUE=LUNG;
RX MEDLINE=96072804; PubMed=7594541;
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
RA Browning J.L., Ware C.F.;
RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
and expression."
RL J. Immunol. 155:5280-5289(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163885; PubMed=8586432;
RA Nakanura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
RA Honjo T.;
RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal

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RT sequence trap and chromosomal mapping.";
RL Genomics 30:312-319(1995).
CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U29173; AAA68964.1; -
CC EMBL: L38423; AAB00846.1; -
CC EMBL: U30798; AAA81334.1; -
CC HSP: P25942; ICDF.
CC MGI: MGI:104875; LTBR.
CC INTERPRO: IPR001368; -
CC PFAM: PF00020; TNFR_G6; 3.
CC PROSITE: PS00652; TNFR_NGFR_1; 2.
CC PROSITE: PS00500; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 415
FT DOMAIN 31 223
FT TRANSMEM 224 244
FT DOMAIN 245 415
FT DOMAIN 42 213
FT REPEAT 42 81
FT REPEAT 82 124
FT REPEAT 125 170
FT REPEAT 171 213
FT DISULFID 43 58
FT DISULFID 59 72
FT DISULFID 62 80
FT DISULFID 83 98
FT DISULFID 101 116
FT DISULFID 104 124
FT DISULFID 126 132
FT DISULFID 139 150
FT DISULFID 142 169
FT DISULFID 172 187
FT CARBOHYD 40 40
FT CARBOHYD 179 179
SQ SEQUENCE 415 AA; 44956 MW; 29B326A566AEF661 CRC64;

Query Match
Best Local Similarity 6.0%; Score 134.5; DB 1; Length 415;
Matches 46; Conservative 28; Mismatches 70; Indels 45; Gaps 8;

QY 47 VPCNQCGPMELSKCEGFGYGEDAQVTCRLHFRKEDWG--FQCKPCPLDCAVVNRFQK-A 104
D 47 VPCNQCGPMELSKCEGFGYGEDAQVTCRLHFRKEDWG--FQCKPCPLDCAVVNRFQK-A 104
D 57 VCCSRPPGFEVFAVC--SRSDQTVCKTCPHNSYNEHNLSTCOLCRPCDIVLGFEEVA 114
QY 105 NCSATSDATCGDCLPGF-----YKTKLVGFQ-----DMCEVPC- 138
D 105 NCSATSDATCGDCLPGF-----YKTKLVGFQ-----DMCEVPC- 138
D 115 PCTSDRKAEC-RCQPGMSCVYLDNECVHCEERLVLCQPGTEAEVDEIMDTVNCVPCK 173
QY 139 -----GDPPEPEPHCASKVNLVKIATASPRDTAL-----AAVICSALATVLLA 184
D 139 -----GDPPEPEPHCASKVNLVKIATASPRDTAL-----AAVICSALATVLLA 184
D 174 PGHFQNTSSPRACQPHTRCEIOGLVEAPGTSYSDTICKNPPPGAMLLALLLSLVLF 233
QY 185 LLILCVYC 193
D 185 LLILCVYC 193
D 234 LLFTTVLAC 242

RESULT 12
LMB1_MOUSE

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LMBL_MOUSE STANDARD; PRT; 1786 AA.
AC P02469;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN).
GN LAMBI-1 OR LAMB-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=87147212; PubMed=3493487;
RA Sasaki M., Kato S., Kohno K., Martin G.R., Yamada Y.;
RT "Sequence of the cDNA encoding the laminin B1 chain reveals a
RT multidomain protein containing cysteine-rich repeats.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:935-939(1987).
RN [2]
RP SEQUENCE OF 1292-1786 FROM N.A.
RX MEDLINE=85051302; PubMed=6209134;
RA Barlow D.P., Green N.M., Kurkinen M., Hogan B.L.M.;
RT "Sequencing of laminin B chain cDNAs reveals C-terminal regions of
RT coiled-coil alpha-helix";
RL EMBO J. 3:2355-2362(1984).
RN [3]
RP SEQUENCE OF 165-172; 539-547 AND 712-719.
RC STRAIN=BALB/C; TISSUE=ENDOTHELIAL CELLS;
RX MEDLINE=97363207; PubMed=9219532;
RA Frieser M., Noeckel H., Pausch F., Roeder C., Hahn A., Deutzmann R.,
RA Sorokin L.M.;
RT "Cloning of the mouse laminin alpha 4 cDNA. Expression in a subset of
RT endothelium.";
RL Eur. J. Biochem. 246:727-735(1997).
CC -!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR. LAMININ
CC IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
CC CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
CC WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
CC -!- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
CC DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
CC TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
CC COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
CC THE BETA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMININ), LAMININ-
CC 2 (MEROSIN), AND LAMININ-6 (K-LAMININ).
CC -!- CELLULAR LOCATION: EXTRACELLULAR.
CC -!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
CC COMPONENT).
CC -!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC -!- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL; M15525; AAA39407.1; ALT_INIT.
DR EMBL; X05212; CAA28839.1; -.
DR PIR; A26413; MMMSB1.
DR HSDP; P03069; 12IM.
DR MGD; MGI:96743; LAMB1-1.
DR INTERPRO; IPR000561; -.
DR INTERPRO; IPR001886; -.
DR INTERPRO; IPR002049; -.
DR PFAM; PF00053; laminin_EGF_13.
DR PFAM; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGF_LAMININ.
DR PROSITE; PS00022; EGF_1; 9.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01246; LAMININ_TYPE_EGF; 11.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;

KW	Laminin EGF-like domain;	Cell adhesion; Repeat; Signal.
FT SIGNAL	1 21	LAMININ BETA-1 CHAIN.
FT CHAIN	22 1786	LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN	22 270	4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN V).
FT DOMAIN	271 540	LAMININ EGF-LIKE 1.
FT DOMAIN	271 334	LAMININ EGF-LIKE 2.
FT DOMAIN	335 397	LAMININ EGF-LIKE 3.
FT DOMAIN	398 457	LAMININ EGF-LIKE 4.
FT DOMAIN	458 509	LAMININ EGF-LIKE 5 (INCOMPLETE).
FT DOMAIN	510 540	LAMININ DOMAIN IV.
FT DOMAIN	541 772	8 X LAMININ EGF-LIKE REPEATS (DOMAIN III).
FT DOMAIN	773 1178	LAMININ EGF-LIKE 6.
FT DOMAIN	773 820	LAMININ EGF-LIKE 7.
FT DOMAIN	821 866	LAMININ EGF-LIKE 8.
FT DOMAIN	867 916	LAMININ EGF-LIKE 9.
FT DOMAIN	917 975	LAMININ EGF-LIKE 10.
FT DOMAIN	976 1027	LAMININ EGF-LIKE 11.
FT DOMAIN	1028 1083	LAMININ EGF-LIKE 12.
FT DOMAIN	1084 1131	LAMININ EGF-LIKE 13.
FT DOMAIN	1132 1178	DOMAIN II.
FT DOMAIN	1179 1397	DOMAIN ALPHA.
FT DOMAIN	1398 1430	DOMAIN I.
FT DOMAIN	1431 1786	COILED COIL (POTENTIAL).
FT DOMAIN	1216 1315	COILED COIL (POTENTIAL).
FT DOMAIN	1368 1388	COILED COIL (POTENTIAL).
FT DOMAIN	1448 1778	BY SIMILARITY.
FT DISULFID	271 280	BY SIMILARITY.
FT DISULFID	273 298	BY SIMILARITY.
FT DISULFID	300 309	BY SIMILARITY.
FT DISULFID	312 332	BY SIMILARITY.
FT DISULFID	335 344	BY SIMILARITY.
FT DISULFID	337 362	BY SIMILARITY.
FT DISULFID	365 374	BY SIMILARITY.
FT DISULFID	377 395	BY SIMILARITY.
FT DISULFID	398 411	BY SIMILARITY.
FT DISULFID	400 426	BY SIMILARITY.
FT DISULFID	428 437	BY SIMILARITY.
FT DISULFID	440 455	BY SIMILARITY.
FT DISULFID	458 472	BY SIMILARITY.
FT DISULFID	460 479	BY SIMILARITY.
FT DISULFID	481 490	BY SIMILARITY.
FT DISULFID	493 507	BY SIMILARITY.
FT DISULFID	773 785	BY SIMILARITY.
FT DISULFID	775 792	BY SIMILARITY.
FT DISULFID	794 803	BY SIMILARITY.
FT DISULFID	806 818	BY SIMILARITY.
FT DISULFID	821 833	BY SIMILARITY.
FT DISULFID	823 840	BY SIMILARITY.
FT DISULFID	842 851	BY SIMILARITY.
FT DISULFID	854 864	BY SIMILARITY.
FT DISULFID	867 876	BY SIMILARITY.
FT DISULFID	869 883	BY SIMILARITY.
FT DISULFID	886 895	BY SIMILARITY.
FT DISULFID	898 914	BY SIMILARITY.
FT DISULFID	917 933	BY SIMILARITY.
FT DISULFID	919 944	BY SIMILARITY.
FT DISULFID	946 955	BY SIMILARITY.
FT DISULFID	958 973	BY SIMILARITY.
FT DISULFID	976 990	BY SIMILARITY.
FT DISULFID	978 997	BY SIMILARITY.
FT DISULFID	1000 1009	BY SIMILARITY.
FT DISULFID	1012 1025	BY SIMILARITY.
FT DISULFID	1084 1096	BY SIMILARITY.
FT DISULFID	1086 1103	BY SIMILARITY.
FT DISULFID	1105 1114	BY SIMILARITY.
FT DISULFID	1117 1129	BY SIMILARITY.
FT DISULFID	1132 1144	BY SIMILARITY.
FT DISULFID	1134 1151	BY SIMILARITY.
FT DISULFID	1153 1162	BY SIMILARITY.
FT DISULFID	1165 1176	INTERCHAIN (PROBABLE).
FT DISULFID	1179 1179	

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FT DISULFID 1182 1182 INTERCHAIN (PROBABLE).
FT DISULFID 1785 1785 INTERCHAIN (PROBABLE).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 519 519 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 677 677 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1041 1041 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1195 1195 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1279 1279 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1336 1336 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1343 1343 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1487 1487 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1533 1533 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1542 1542 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1643 1643 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 1531 1534 SGNA -> N (IN REF. 2).
FT CONFLICT 1749 1749 D -> N (IN REF. 2).
SQ SEQUENCE 1786 AA; 196904 MW; 846671B/F41A474 CRC64;

Query Match 5.9%; Score 134; DB 1; Length 1786;
Best Local Similarity 20.9%; Pred No. 0.013;
Matches 84; Conservative 32; Mismatches 124; Indels 162; Gaps 24;

QY 21 GYLSKVTCTGDCRQDFRDRSGNCP-----CNQCGPMGSMELSKCEGFGYGED----- 69
Db 779 GSLSVCDPNQGQC-----CRPNVVGRTCNRCAPGT-----FGFGPGCKPC 821
QY 70 -----AQCVCRLHREK-----EDWGFQCKPC-----LDCAVVR 100
Db 822 DCHLQGSASFADAITGQCHFCGFIYARQCDRLCPGYWGFSPQCQNGCHALDCTVT- 880
QY 101 FOKANGSATSDAI-----CGDCLPGFYRKTLVGFQDMCVPCGDDPPP-----YEPHCAS 151
Db 881 ---GELSCQDYTGHCNRCLAGIY-GPIITGSD-HCRPCPCPDGPGSGRQFARSCVQ 935
QY 152 KVNVLXIATASPRDTAAVTCASALATVLLALILCVYKRPMEKKPSWLSRSDI 211
Db 936 DPVTQLACVC-----DPGVIGSRCD-----CASGFGFNPSDFGGSCQPC 976
QY 212 QYN-----GSELSCL-----DRPOLHEYAH-----RAC----- 234
Db 977 QCHNHNTDTPACDKDGTGRCLKCLYHTGDHCLQCYGYGDALRQDCRCKVCNVLGTV 1036
QY 235 -----CQCRDSVQ-TCGPVRLPLSPMCCEACSPNPATL-----GCGVHSAASIAQARN 281
Db 1037 KEHCNSDCHCDKATQCCLP-NVIGQNC--DRCAPNTWLQASGTGCGPCNCNA--AHS 1091
QY 282 AGPAGEMVPTFFGSLTQSGEFSFSDAMPLQMPMGDNISFC 323
Db 1092 FGPS-----CNEFTGQCQCMGP-FGGRTCSEC 1117

RESULT 13
LMB2_MOUSE
ID LMB2_MOUSE STANDARD; PRT; 1799 AA.
AC Q61292; Q62182;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE LAMININ BETA-2 CHAIN PRECURSOR.
GN LAMB2 OR S-LAM OR LAMS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=129/J;
RX MEDLINE=96278760; PubMed=8662701;
RA Durkin M.E., Gautam M., Loebel S., Sanes J.R., Merlie J.P.,
RA Albrechtsen R., Wever U.M.;
RT "Structural organization of the human and mouse laminin beta2 chain
genes, and alternative splicing at the 5' end of the human

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transcript.";
J. Biol. Chem. 271:13407-13416(1996).
[2]
SEQUENCE OF 348-428 FROM N.A.
RC TISSUE=LUNG;
RX MEDLINE=94319092; PubMed=8043959;
RA Aberdam D., Galliano M.F., Mattei M.-G., Ortonne J.P., Meneguzzi G.;
RT "S-laminin gene (lams) maps to F1 band of mouse chromosome 9.";
RN Mamm. Genome 5:393-394(1994).
[3]
FUNCTION.
RP STRAIN=129/J;
RC MEDLINE=95191650; PubMed=7885444;
RA Noakes P.G., Gautam M., Mudd J., Sanes J.R., Merlie J.P.;
RT "Aberrant differentiation of neuromuscular junctions in mice lacking
s-laminin/laminin beta 2.";
RN Nature 374:258-262(1995).
RP -!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ
IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
-!- FUNCTION: LAMININ-3 (S-LAMININ) REGULATES THE FORMATION OF MOTOR
NERVE TERMINALS.
-!- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4
(S-MEROSIN), AND LAMININ-7 (KS-LAMININ).
-!- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
MEMBRANES (MAJOR COMPONENT).
-!- TISSUE SPECIFICITY: NEUROMUSCULAR SYNAPSE AND KIDNEY GLOMERULUS.
-!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
-!- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.
-!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
-!- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
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EMBL; U43541; AAC53535.1; -
EMBL; U42624; AAC53535.1; JOINED.
EMBL; X75928; CAA53532.1; -
HSSP; P02468; 1KLO.
MGD; MGI:99916; LAMB2.
INTERPRO; IPR000561; -
INTERPRO; IPR001886; -
INTERPRO; IPR002049; -
PFAM; PF00053; laminin_EGF; 13.
PFAM; PF00055; laminin_Nterm; 1.
PRINTS; PR00011; EGF_LAMININ.
PROSITE; PS00022; EGF_1; 10.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
KW Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT SIGNAL 1 35 POTENTIAL.
FT CHAIN 36 1799 LAMININ BETA-2 CHAIN.
FT DOMAIN 36 283 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 284 555 4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
V).
FT DOMAIN 286 349 LAMININ EGF-LIKE 1.
FT DOMAIN 350 412 LAMININ EGF-LIKE 2.
FT DOMAIN 413 472 LAMININ EGF-LIKE 3.
FT DOMAIN 473 524 LAMININ EGF-LIKE 4.
FT DOMAIN 525 555 LAMININ EGF-LIKE 5 (INCOMPLETE).

```


RN [4] SEQUENCE OF 1-1400 FROM N.A.
 RP MEDLINE=87004550; PubMed=3019665;
 RA Verweij C.L., Diergaarde P.J., Hart M., Pannekoek H.;
 RT "Full-length von Willebrand factor (vWF) cDNA encodes a highly
 RT repetitive protein considerably larger than the mature vWF subunit.";
 RL EMBO J. 5:1839-1847(1986).
 RN [5] ERRATUM.
 RP Verweij C.L., Diergaarde P.J., Hart M., Pannekoek H.;
 RL EMBO J. 5:3074-3074(1986).
 RN [6] SEQUENCE OF 764-2813.
 RP MEDLINE=86269895; PubMed=3524673;
 RA Titani K., Kumar S., Takio K., Ericsson L.H., Wade R.D., Ashida K.,
 RA Walsh K.A., Choquet M.W., Sadler J.E., Fujikawa K.;
 RT "Amino acid sequence of human von Willebrand factor.";
 RL Biochemistry 25:3171-3184(1986).
 RN [7] SEQUENCE OF 781-1424 FROM N.A.
 RP MEDLINE=86269894; PubMed=3488076;
 RA Shelton-Inloes B.B., Titani K., Sadler J.E.;
 RT "cDNA sequences for human von Willebrand factor reveal five types of
 RT repeated domains and five possible protein sequence polymorphisms.";
 RL Biochemistry 25:3164-3171(1986).
 RN [8] SEQUENCE OF 764-873 AND 1289-2813 FROM N.A.
 RP MEDLINE=86016708; PubMed=2864688;
 RA Sadler J.E., Shelton-Inloes B.B., Sorace J.M., Harlan J.M.,
 RA Titani K., Davie E.W.;
 RT "Cloning and characterization of two cDNAs coding for human von
 RT Willebrand factor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:6394-6398(1985).
 RN [9] SEQUENCE OF 990-1947 FROM N.A.
 RP MEDLINE=91105089; PubMed=1988024;
 RA Mancuso D.J., Tuley E.A., Westfield L.A., Lester-Mancuso T.L.,
 RA Le-Beau M.M., Sorace J.M., Sadler J.E.;
 RT "Human von Willebrand factor gene and pseudogene: structural analysis
 RT and differentiation by polymerase chain reaction.";
 RL Biochemistry 30:253-269(1991).
 RN [10] SEQUENCE OF 2731-2813 FROM N.A.
 RP MEDLINE=85269603; PubMed=3875078;
 RA Verweij C.L., de Vries C.J.M., Distel B., van Zonneveld A.-J.,
 RA Geurts van Kessel A., van Mourik J.A., Pannekoek H.;
 RT "Construction of cDNA coding for human von Willebrand factor using
 RT antibody probes for colony-screening and mapping of the chromosomal
 RT gene.";
 RL Nucleic Acids Res. 13:4699-4717(1985).
 RN [11] SEQUENCE OF 1-177 FROM N.A.
 RP MEDLINE=88111704; PubMed=2828057;
 RA Bonthron D., Orkin S.H.;
 RT "The human von Willebrand factor gene. Structure of the 5' region.";
 RL Eur. J. Biochem. 171:51-57(1988).
 RN [12] SEQUENCE OF 2621-2813 FROM N.A.
 RP MEDLINE=85244588; PubMed=3874428;
 RA Ginsburg D., Handin R.I., Bonthron D.T., Donlon T.A., Bruns G.A.P.,
 RA Latt S.A., Orkin S.H.;
 RT "Human von Willebrand factor (vWF): isolation of complementary DNA
 RT (cDNA) clones and chromosomal localization.";
 RL Science 228:1401-1406(1985).
 RN [13] SEQUENCE OF 2731-2813 FROM N.A.
 RP MEDLINE=85201687; PubMed=3873280;
 RA Lynch D.C., Zimmerman T.S., Collins C.J., Brown M., Morin M.J.,
 RA Ling E.H., Livingston D.M.;
 RT "Molecular cloning of cDNA for human von Willebrand factor:
 RT authentication by a new method.";
 RL Cell 41:49-56(1985).
 RN [14]

RP REVISIONS.
 RA Lynch D.C.;
 RL Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.
 RN [15] SEQUENCE OF 2731-2813 FROM N.A.
 RP MEDLINE=87260814; PubMed=3496594;
 RA Collins C.J., Underdahl J.P., Levene R.B., Ravera C.P.,
 RA Morin M.J., Dombalagian M.J., Ricca G., Livingston D.M.,
 RA Lynch D.C.;
 RT "Molecular cloning of the human gene for von Willebrand factor and
 RT identification of the transcription initiation site.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4393-4397(1987).
 RN [16] DISULFIDE BONDS.
 RP MEDLINE=88163465; PubMed=3502076;
 RA Marti T., Rosselet S.J., Titani K., Walsh K.A.;
 RT "Identification of disulfide-bridged substructures within human von
 RT Willebrand factor.";
 RL Biochemistry 26:8099-8109(1987).
 RN [17] STRUCTURE OF CARBOHYDRATES.
 RP MEDLINE=86274702; PubMed=3089784;
 RA Samor B., Michalski J.C., Debray H., Mazurier C., Goudemand M.,
 RA van Halbeek H., Vliegthart J.F.G., Montreuil J.;
 RT "Primary structure of a new tetraantennary glycan of the N-
 RT acetylactosaminic type isolated from human factor VIII/von
 RT Willebrand factor.";
 RL Eur. J. Biochem. 158:295-298(1986).
 RN [18] X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1261-1468.
 RP MEDLINE=98221174; PubMed=9553097;
 RA Emsley J., Cruz M., Handin R., Liddington R.;
 RT "Crystal structure of the von Willebrand factor A1 domain and
 RT implications for the binding of platelet glycoprotein Ib.";
 RL J. Biol. Chem. 273:10396-10401(1998).
 RN [19] X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 1685-1873.
 RP MEDLINE=97472999; PubMed=9331419;
 RA Huizinga E.G., Martijn van der Plas R., Kroon J., Sixma J.J., Gros P.;
 RT "Crystal structure of the A3 domain of human von Willebrand factor:
 RT implications for collagen binding.";
 RL Structure 5:1147-1156(1997).
 RN [20] X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 1686-1872.
 RP MEDLINE=97460108; PubMed=9312128;
 RA Bienkowska J., Cruz M., Atiemo A., Handin R., Liddington R.;
 RT "The von Willebrand factor A3 domain does not contain a metal ion-
 RT dependent adhesion site motif.";
 RL J. Biol. Chem. 272:25162-25167(1997).
 RN [21] VARIANTS TRP-1597 AND ASP-1607.
 RP MEDLINE=89264495; PubMed=2786201;
 RA Ginsburg D., Konkle B.A., Gill J.C., Montgomery R.R.,
 RA Bockenstedt P.L., Johnson T.A., Yang A.Y.;
 RT "Molecular basis of human von Willebrand disease: analysis of
 RT platelet von Willebrand factor mRNA.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:3723-3727(1989).
 RN [22] VARIANT THR-1628.
 RP MEDLINE=91196734; PubMed=1673047;
 RA Iannuzzi M.C., Hidaka N., Boehnke M., Bruck M.E., Hanna W.T.,
 RA Collins F.S., Ginsburg D.;
 RT "Analysis of the relationship of von Willebrand disease (vWD) and
 RT hereditary hemorrhagic telangiectasia and identification of a
 RT potential type IIA vWD mutation (Ile865 to Thr).";
 RL Am. J. Hum. Genet. 48:757-763(1991).
 RN [23] VARIANTS NORMANDY-2 AND NORMANDY-3.
 RP MEDLINE=92001464; PubMed=1832934;
 RA Gaucher C., Mercier B., Jorleux S., Oufkir D., Mazurier C.;
 RT "Identification of two point mutations in the von Willebrand factor
 RT gene of three families with the 'Normandy' variant of von Willebrand
 RT disease.";

```
RL Br. J. Haematol. 78:506-514(1991).
RN [24]
RP VARIANT CYS-1308.
RX MEDLINE-92104315; PubMed=1761120;
RA Donner M., Andersson A.-M., Kristoffersson A.-C., Nilsson I.M.,
RA Dahlback B., Holmberg L.;
RT "An Arg545-->Cys345 substitution mutation of the von Willebrand
RT factor in type IIB von Willebrand's disease.";
RN Eur. J. Haematol. 47:342-345(1991).
RN [25]
RP VARIANTS TRP-1306; CYS-1308 AND PRO-1613.
RX MEDLINE-91185601; PubMed=2010538;
RA Randi A.M., Rabinowitz I., Mancuso D.J., Mannucci P.M., Sadler J.E.;
RT "Molecular basis of von Willebrand disease type IIB. Candidate
RT mutations cluster in one disulfide loop between proposed platelet
RT glycoprotein Ib binding sequences.";
RN J. Clin. Invest. 87:1220-1226(1991).
RN [26]
RP VARIANTS TRP-1306; CYS-1308; MET-1316; GLN-1341 AND HIS-1399.
RX MEDLINE-91185602; PubMed=1672694;
RA Cooney K.A., Nichols W.C., Bruck M.E., Bahou W.F., Shapiro A.D.,
Query Match 5.9%; Score 133.5; DB 1; Length 2813;
Best Local Similarity 21.4%; Pred. No. 0.023;
Matches 78; Conservative 38; Mismatches 107; Indels 141; Gaps 19;
QY 44 GNCVPT---CNCQCPGMELSKGCGFGYGEDAQCVTCRLHFKEDWGFKCKPCLDCAVVR 100
DB 2246 GSCVPEACTQC-----IGEDGV-----QHGFLEAW-VPDHPQCICICLSG 2286
QY 101 FQKANS-----TSDA-ICGDCPLGPRYKTKLVGFODMEC----VPCGDPPPPPYEPHCAS 151
DB 2287 -RVNCTTQPCPTAKAPTGCGLCEVARLRQNAQCCPEYECVCDPVSCLDLP---VPHCER 2342
QY 152 KYNLVKIATSTASPRDTALAAVICSALATVLLALLILVIYCKRQPMKKPWSLSRQDI 211
DB 2343 -----GLQPTLNPGE-----CRPNP----- 2358
QY 212 QYNGSELCLDRPQLRHEAHACCCQCRDVSOTGVRLLPSM-----CCCEE---ACSPNP 264
DB 2359 -----TCACRKE-----ECKRVSPSPCPHPR-LPTLRKTQCCDEYECACNCYN 2400
QY 265 ATLCGCVHSAASLQARNAGPAGWVTFPGSLTQSCGFESDAWPL----- 310
DB 2401 STVSCPLGLVLAATNDCG-----CTTTTCLPKVCHVRSTIYPVGFWEBCDVCCTCT 2454
QY 311 -MNPNGDNISFCDSP-----ELTGEDIHSLNPELESSTSLDSSNQ 353
DB 2455 DMEDAVMGLRVAQCSOKPCEDSCRSRGFTVYLHEGECGRCLPSACEVVTGSPRGDSQSSW 2514
QY 354 DLVG 357
DB 2515 KSVG 2518
RESULT 15
TSPI_MOUSE STANDARD; PRT; 1170 AA.
AC P35441.
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE THROMBOSPONDIN 1 PRECURSOR.
GN THBS1 OR TSPI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RX MEDLINE-92128941; PubMed=1774063;
RA Lawler J., Duquette M., Ferro P., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A.;
RT "Characterization of the murine thrombospondin gene.";
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KW Glycoprotein: Cell adhesion; Calcium-binding; Heparin-binding; Repeat;
 KW EGF-like domain; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 1170
 FT DOMAIN 19 232
 FT DOMAIN 316 373
 FT DOMAIN 379 548
 FT DOMAIN 549 690
 FT DOMAIN 723 950
 FT DOMAIN 951 1170
 FT REPEAT 379 430
 FT REPEAT 435 491
 FT REPEAT 492 548
 FT DOMAIN 549 587
 FT DOMAIN 588 645
 FT DOMAIN 646 690
 FT REPEAT 723 758
 FT REPEAT 759 781
 FT REPEAT 817 840
 FT REPEAT 841 878
 FT REPEAT 879 914
 FT REPEAT 915 950
 FT SITE 926 928
 FT DISULFID 270 270
 FT DISULFID 274 274
 FT DISULFID 551 562
 FT DISULFID 556 572
 FT DISULFID 575 586
 FT DISULFID 592 608
 FT DISULFID 599 617
 FT DISULFID 620 644
 FT DISULFID 650 663
 FT DISULFID 657 675
 FT DISULFID 678 689
 FT CARBOHYD 248 248
 FT CARBOHYD 360 360
 FT CARBOHYD 708 708
 FT CARBOHYD 1067 1067
 FT CONFLICT 1025 1025
 SQ SEQUENCE 1170 AA; 129646 MW; 0443E493615E7F06 CRC64;

Query Match 5.9%; Score 132.5; DB 1; Length 1170;
 Best Local Similarity 21.0%; Pred. No. 0.01;
 Matches 88; Conservative 39; Mismatches 141; Indels 151; Gaps 25;

QY 26 KVTCTGCRQGFDRSGNCVPCNQCQPG-----MELSKGCGFY----- 66
 DB 350 KVSCLPMPSCNATVPD--GEC--CPRCWPDSADDDGWSHSPWSEWTSATCGNGIQGRS 405
 QY 67 -----GEDAQVTCRLH---REFEDWGFQKCKPCLDCA-----VYVREFKAN-- 105
 DB 406 CDSLNNRCGSSVQTRTCHIQECDKRFKQGGWSHSPWSSCVTCGDGVITRILCNPS 465
 QY 106 -----CSATSDAICGCLPGFYRKTCL 127
 DB 466 SPQWNGKPCGEARETRACKKADCPINGGWPSPWDICSVT-----CGG---GVQRESRL 518
 QY 128 VGFQDMCEVCGDPPPY-EPHCASKVNLVKIATASSPRDTALAIVICSALATVLLALL 186
 DB 519 -----CNPPTQFGKDKCVGDTENQVCNKQDCPIDGCLSNP-CFAGAK----- 561
 QY 187 ILCVIYCKRFMEKPSLSRSDIOYNGSELSCLDRLPHE-----YAHRAACCOCRR-D 240
 DB 562 --CYSY-----PDGSKWKGACPPGSGNGIQCKVDECKEVPDCAFNHNGEHRKNTD 612
 QY 241 SVQTC--GPVRLFPS-----MCEEACSP-NPATLG---CGVHSAASLOARNAGP 284
 DB 613 PGYNCLCPPRFTGSPFGRGVEHAMANKQVCKPRNCTDGTDCNKNKACNYLGHYSDP 672
 QY 285 --AGENVPTFTGSLTQICGEFS--DAWPLMNPMPGDNISF-----CDSYBELTGED 333

Db 673 MYRCECKPGVAGN--GIICGEDTDLDGWP-NENLVCVANATYHCKKDNCPNLPNSQOED 728

Search completed: February 16, 2001, 21:09:26
 Job time: 231 sec

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OM protein - protein search, using sw model

Run on: February 16, 2001, 21:05:05 ; Search time 53.31 seconds
 (without alignments)
 916.820 Million cell updates/sec

Title: US-09-380-276A-4
 Perfect score: 2255
 Sequence: 1 MALKVLEQEKFTFTLLVLL.....LDQSGAIHPATQTSIQEA 417

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPTREMBL_15:*
- 2: sp_archaea:*
- 3: sp_bacteria:*
- 4: sp_fungi:*
- 5: sp_human:*
- 6: sp_invertebrate:*
- 7: sp_mammal:*
- 8: sp_mhc:*
- 9: sp_organelle:*
- 10: sp_phage:*
- 11: sp_plant:*
- 12: sp_rodent:*
- 13: sp_virus:*
- 14: sp_vertebrate:*
- 15: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2237	99.2	423	4 Q9NS68	Q9ns68 homo sapien
2	2221	98.5	423	4 Q9NZV2	Q9nzv2 homo sapien
3	1565.5	69.4	416	11 Q9JH6	Q9jh6 mus musculus
4	1563.5	69.3	416	11 Q9JLL3	Q9jll3 mus musculus
5	1472.5	65.3	348	11 Q9QXW7	Q9qxw7 mus musculus
6	977	43.3	214	11 Q9JHF1	Q9jhf1 mus musculus
7	725	32.2	150	11 Q9JLL2	Q9jll2 mus musculus
8	197	8.7	448	11 Q9R187	Q9r187 mus musculus
9	191	8.5	448	4 Q9UNE0	Q9une0 homo sapien
10	191	8.5	448	4 Q9UND9	Q9und9 homo sapien
11	170.5	7.6	387	13 Q9PVD4	Q9pvd4 xenopus lae
12	144.5	6.4	430	6 Q9N092	Q9n092 macaca fasc
13	142	6.3	417	11 Q9Z0W1	Q9z0w1 mus musculus
14	142	6.3	426	4 O14865	O14865 homo sapien
15	137.5	6.1	186	12 Q72735	Q72735 cowpox viru
16	136	6.0	625	11 O35305	O35305 mus musculus
17	134.5	6.0	3396	5 Q9VM55	Q9vm55 drosophila
18	134	5.9	186	12 Q9YP87	Q9yp87 cowpox viru
19	134	5.9	277	4 O14866	O14866 homo sapien

20	134	5.9	348	12	O57277	057277 monkeypox v
21	134	5.9	348	12	O57103	057103 monkeypox v
22	134	5.9	348	12	O57108	057108 monkeypox v
23	133.5	5.9	350	12	O57123	057123 cowpox viru
24	133	5.9	543	5	Q9VJ05	Q9vj05 drosophila
25	133	5.9	620	5	Q9NKD8	Q9nk8 drosophila
26	132.5	5.9	3680	5	Q9VR08	Q9vr08 drosophila
27	131.5	5.8	349	12	O57291	057291 monkeypox v
28	131.5	5.8	349	12	O57099	057099 monkeypox v
29	131.5	5.8	349	12	O57100	057100 monkeypox v
30	131.5	5.8	349	12	O57101	057101 monkeypox v
31	131.5	5.8	349	12	O57102	057102 monkeypox v
32	130	5.8	186	12	Q9WJB4	Q9wj4 vaccinia vi
33	129.5	5.7	1254	13	Q9YHU2	Q9yhu2 brachydanio
34	128	5.7	347	12	O57115	057115 cowpox viru
35	128	5.7	355	12	Q85308	Q85308 cowpox viru
36	128	5.7	401	13	Q9PRG7	Q9prg7 xenopus lae
37	127.5	5.7	349	12	O57111	057111 variola vir
38	127	5.6	1114	11	Q9JKW7	Q9jkw7 mus musculus
39	127	5.6	1650	11	Q9QVT6	Q9qvt6 rattus sp.
40	127	5.6	1792	13	O57484	057484 gallus gall
41	127	5.6	1827	5	Q20535	Q20535 caenorhabdi
42	126.5	5.6	380	4	O00280	O00280 homo sapien
43	126.5	5.6	1394	5	Q9VS89	Q9vs89 drosophila
44	126	5.6	349	12	O57305	057305 cowpox viru
45	126	5.6	350	12	O57116	057116 cowpox viru

ALIGNMENTS

RESULT 1
 Q9NS68 PRELIMINARY; PRT; 423 AA.
 AC Q9NS68;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE HTROY.
 GN HTROY.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,
 RA Senba E., Kitamura T.;
 RT "TROY, a newly identified member of the tumor necrosis factor receptor
 RT superfamily, exhibits a homology with Edar and is expressed in
 RT embryonic skin and hair follicles";
 RL J. Biol. Chem. 275:20742-20747(2000).
 DR EMBL; AB040434; BAB03269.1; -;
 SQ SEQUENCE 423 AA; 46015 MW; B5891CEA9ED45361 CRC64;

Query Match 99.2%; Score 2237; DB 4; Length 423;
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Db	121	FYRKTKLVCFQDMECVPCGDPDPPEPHCASKNLVKIATASSPPDPTALAAVICSALAT 180	
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181 VLLALLILCVYKROFMKPSWSLSRSDIQYNGSELSCFDRPQLHEYAHRACCCRRD 240
QY 241 SVOTCGVRLPSCMCCEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Db 241 SVOTCGVRLPSCMCCEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
QY 301 CGFSDAWPLMQNPMGMDNISFCDSYPELTGEDIHSLNPELESSTLSDNSSODLVGGAV 360
Db 301 CGFSDAWPLMQNPMGMDNISFCDSYPELTGEDIHSLNPELESSTLSDNSSODLVGGAV 360
QY 361 PVQSHSENFTAATDLSRYNNLTVESASTQDALTMRSQLDQESGAIHPATQTSIQ 415
Db 361 PVQSHSENFTAATDLSRYNNLTVESASTQDALTMRSQLDQESGAIHPATQTSIQ 415

RESULT 2
Q9NZV2
ID Q9NZV2 PRELIMINARY; PRT; 423 AA.
AC Q9NZV2;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (T-EMBLrel. 15, Last annotation update)
DE TAJ-ALPHA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
RT Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-
RT Independent Cell Death.";
RL J. Biol. Chem. 275:15336-15342(2000).
DR EMBL; AF167555; AAF1828.1; -.
SQ SEQUENCE 423 AA; 46071 MW; BB7C9917132A4B2F CRC64;

Query Match 98.5%; Score 2221; DB 4; Length 423;
Best Local Similarity 98.8%; Pred. No. 8.8e-198;
Matches 409; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MALKVLLLEQEKTFETLLVLLGYLSCKVTCTGDCRQOEFRDRSGNCVPCNQCGPMELSK 60
Db 1 MALKVLLLEQEKTFETLLVLLGYLSCKVTCTGDCRQOEFRDRSGNCVPCNQCGPMELSK 60
QY 61 ECGFGYGEDAQCVTLRHREKEDWGFKCKPCLDCAVVRNFRKANCATSATDAICGDCPLG 120
Db 61 ECGFGYGEDAQCVTLRHREKEDWGFKCKPCLDCAVVRNFRKANCATSATDAICGDCPLG 120
QY 121 FYRKTCLVGFQDMCEVPCGDPPEPPHPCASKVNLVKIASTASSPRDTALAAVICSALAT 180
Db 121 FYRKTCLVGFQDMCEVPCGDPPEPPHPCASKVNLVKIASTASSPRDTALAAVICSALAT 180
QY 181 VLLALLILCVYKROFMKPSWSLSRSDIQYNGSELSCFDRPQLHEYAHRACCCRRD 240
Db 181 VLLALLILCVYKROFMKPSWSLSRSDIQYNGSELSCFDRPQLHEYAHRACCCRRD 240
QY 241 SVOTCGVRLPSCMCCEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Db 241 SVOTCGVRLPSCMCCEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
QY 301 CGFSDAWPLMQNPMGMDNISFCDSYPELTGEDIHSLNPELESSTLSDNSSODLVGGAV 360
Db 301 CGFSDAWPLMQNPMGMDNISFCDSYPELTGEDIHSLNPELESSTLSDNSSODLVGGAV 360
QY 361 PVQSHSENFTAATDLSRYNNLTVESASTQDALTMRSQLDQESGAIHPATQTSIQ 415
Db 361 PVQSHSENFTAATDLSRYNNLTVESASTQDALTMRSQLDQESGAIHPATQTSIQ 415

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RESULT 3

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Q9JHH6
ID Q9JHH6 PRELIMINARY; PRT; 416 AA.
AC Q9JHH6;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (T-EMBLrel. 15, Last annotation update)
DE TROY.
GN TROY.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Senba E., Kitamura T.;
RT "TROY, a newly identified member of the tumor necrosis factor receptor
RT superfamily, exhibits a homology with Edar and is expressed in
RT embryonic skin and hair follicles.";
RL J. Biol. Chem. 275:20742-20747(2000).
DR EMBL; AB040432; BAB03267.1; -.
SQ SEQUENCE 416 AA; 45265 MW; 9BDC7C7A2D6A9C47 CRC64;

Query Match 69.4%; Score 1565.5; DB 11; Length 416;
Best Local Similarity 70.4%; Pred. No. 4.9e-137;
Matches 295; Conservative 35; Mismatches 84; Indels 5; Gaps 3;

QY 1 MALKVLLLEQEKTFETLLVLLGYLSCKVTCTGDCRQOEFRDRSGNCVPCNQCGPMELSK 60
Db 1 MALKVLLLEQEKTFETLLVLLGYLSCKVTCTGDCRQOEFRDRSGNCVPCNQCGPMELSK 60
QY 61 ECGFGYGEDAQCVTLRHREKEDWGFKCKPCLDCAVVRNFRKANCATSATDAICGDCPLG 120
Db 61 ECGFGYGEDAQCVTLRHREKEDWGFKCKPCLDCAVVRNFRKANCATSATDAICGDCPLG 120
QY 121 FYRKTCLVGFQDMCEVPCGDPPEPPHPCASKVNLVKIASTASSPRDTALAAVICSALAT 180
Db 121 FYRKTCLVGFQDMCEVPCGDPPEPPHPCASKVNLVKIASTASSPRDTALAAVICSALAT 180
QY 181 VLLALLILCVYKROFMKPSWSLSRSDIQYNGSELSCFDRPQLHEYAHRACCCRRD 240
Db 181 VLLALLILCVYKROFMKPSWSLSRSDIQYNGSELSCFDRPQLHEYAHRACCCRRD 240
QY 241 SVOTCGVRLPSCMCCEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Db 241 SVOTCGVRLPSCMCCEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
QY 301 CGFSDAWPLMQNPMGMDNISFCDSYPELTGEDIHSLNPELESSTLSDNSSODLVGGAV 360
Db 301 CGFSDAWPLMQNPMGMDNISFCDSYPELTGEDIHSLNPELESSTLSDNSSODLVGGAV 360
QY 361 PVQSHSENFTAATDLSRYNN--TLVESASTQDALTMRSQLDQESGAIHPATQTSIQ 417
Db 359 -ALESSGNVSESTSPRHGDTGTWQTLAQDAQRTPSQGGWEDRENINLAMPATFQDA 416

RESULT 4
Q9JLL3
ID Q9JLL3 PRELIMINARY; PRT; 416 AA.
AC Q9JLL3;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (T-EMBLrel. 15, Last annotation update)
DE TAJ-ALPHA LONG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,

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RT Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-
independent Cell Death."
J. Biol. Chem. 275:15336-15342(2000).
DR EMBL: AAF167553; AAF1825.1; -
SQ SEQUENCE 416 AA; 45294 MW; 19CA2B75DD7B9D49 CRC64;

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Query Match          69.3%; Score 1563.5; DB 11; Length 416;
Best Local Similarity 70.4%; Pred. No. 7.5e-137;
Matches 295; Conservative 34; Mismatches 85; Indels 5; Gaps 3;

QY 1 MALKVLEQEKTFLLVLLGLYSCKVTCETGDCRQOEFRDRSGNCVPCNCGPGMELSK 60
DB 1 MALKVLP LHRVT LFAAILFLHLACKVSCETGDCRQOEFKDRSGNCVLCKQCGPGMELSK 60

QY 61 ECGFGYGEDAOCVTCRLHREFKEDWGFKCKPCLDCAVNVRFKANCATSDAICGDCPLG 120
DB 61 ECGFGYGEDAQCPCPRHREFKEDWGFKCKPCADCALVNVRFKANCSTSDAVCGDCPLG 120

QY 121 FYRKTGLVGFQDMCVPCGDDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
DB 121 FYRKTGLVGFQDMCVPCGDDPPPPYEPHCASKVNLVKISSTVSSPRDTALAAVICSALAT 180

QY 181 VLLALLILCVYCKQFMEKPSWLSRSDIQYNGSELSCLDRLPOLHEYAHRACCCRRD 240
DB 181 VLLALLILCVYCKQFMEKPSWLSRSDIQYNGSELSCFDQPRLRHCAHRAACCCYHRD 240

QY 241 SVOTCGPVRLPSSMCCEACSPNPATLGGVHSAASLQARNAGPAGVMVPTFFGSLTOSI 300
DB 241 SAPMGPVHLIPSLCCCEARSARAVLGGGLSRPTTLQERNPASVGNWTPAFFGSVSRSI 300

QY 301 CGEFSDAWPLMGNPMGNDISFCDSPYELTGEDIHSLNPEL 341
DB 301 CAEFSDAWPLMGNPLGGDS-SLSDSYPELTGDTNLSNPEM 340

QY 361 PVQSHSENFATDLSRYNN--TLVESASTQDALWRSQDOESGAIHPATQTSLOEA 417
DB 359 -ALESSGNVSESTDSPRHGDTGVMEQTIAQDARTPSQGWEDRENLMAMPTAFQDA 416

RESULT 5
QYQXW7 PRELIMINARY; PRT; 348 AA.
AC Q9QXW7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE TNFRSF19.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Hu S., Tamada K., Ni J., Vincenz C., Chen L.;
RT "Characterization of TNFRSF19, a novel member of tumor necrosis factor
RL receptor superfamily."
RL Genomics 62:103-107(1999).
DR EMBL: AAF173166; AAF19795.1; -
DR INTERPRO: IPR001368; -
DR PFAM: PF00020; TNFR_C6; 2.
DR PROSITE: PS00052; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE: PS00050; TNFR_NGFR_2; 1.
SQ SEQUENCE 348 AA; 38450 MW; 013C799638F8E333 CRC64;
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Query Match          65.3%; Score 1472.5; DB 11; Length 348;
Best Local Similarity 77.7%; Pred. No. 1.7e-128;
Matches 265; Conservative 24; Mismatches 51; Indels 1; Gaps 1;

QY 1 MALKVLEQEKTFLLVLLGLYSCKVTCETGDCRQOEFRDRSGNCVPCNCGPGMELSK 60
DB 1 MALKVLP LHRVT LFAAILFLHLACKVSCAGDCRQOEFKDRSGNCVLCKQCGPGMELSK 60
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QY 61 ECGFGYGEDAOCVTCRLHREFKEDWGFKCKPCLDCAVNVRFKANCATSDAICGDCPLG 120
DB 61 ECGFGYGEDAQCPCPRHREFKEDWGFKCKPCADCALVNVRFKANCSTSDAVCGDCPLG 120

QY 121 FYRKTGLVGFQDMCVPCGDDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
DB 121 FYRKTGLVGFQDMCVPCGDDPPPPYEPHCASKVNLVKISSTVSSPRDTALAAVICSALAT 180

QY 181 VLLALLILCVYCKQFMEKPSWLSRSDIQYNGSELSCLDRLPOLHEYAHRACCCRRD 240
DB 181 VLLALLILCVYCKQFMEKPSWLSRSDIQYNGSELSCFDQPRLRHCAHRAACCCYHRD 240

QY 241 SVOTCGPVRLPSSMCCEACSPNPATLGGVHSAASLQARNAGPAGVMVPTFFGSLTOSI 300
DB 241 SAPMGPVHLIPSLCCCEARSARAVLGGGLSRPTTLQERNPASVGNWTPAFFGSVSRSI 300

QY 301 CGEFSDAWPLMGNPMGNDISFCDSPYELTGEDIHSLNPEL 341
DB 301 CAEFSDAWPLMGNPLGGDS-SLSDSYPELTGDTNLSNPEM 340

RESULT 6
QYQJHF1 PRELIMINARY; PRT; 214 AA.
AC Q9JHF1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE DTROY (TAJ-ALPHA SHORT).
GN DTROY.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Senba E., Kitamura T.;
RT "TROY, a newly identified member of the tumor necrosis factor receptor
RT superfamily, exhibits a homology with Eder and is expressed in
RT embryonic skin and hair follicles."
RL J. Biol. Chem. 275:20742-20747(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Eby M.T., Jamin A., Kumar A., Sharma K., Chaudhary P.M.;
RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
RT Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-
RT independent Cell Death."
RL J. Biol. Chem. 275:15336-15342(2000).
DR EMBL: AB040433; BAB03268.1; -
DR EMBL: AAF167553; AAF1825.1; -
SQ SEQUENCE 214 AA; 23564 MW; ECC63981C37482B8 CRC64;
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Query Match          43.3%; Score 977; DB 11; Length 214;
Best Local Similarity 84.6%; Pred. No. 8e-83;
Matches 176; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

QY 1 MALKVLEQEKTFLLVLLGLYSCKVTCETGDCRQOEFRDRSGNCVPCNCGPGMELSK 60
DB 1 MALKVLP LHRVT LFAAILFLHLACKVSCETGDCRQOEFKDRSGNCVLCKQCGPGMELSK 60

QY 61 ECGFGYGEDAOCVTCRLHREFKEDWGFKCKPCLDCAVNVRFKANCATSDAICGDCPLG 120
DB 61 ECGFGYGEDAQCPCPRHREFKEDWGFKCKPCADCALVNVRFKANCSTSDAVCGDCPLG 120

QY 121 FYRKTGLVGFQDMCVPCGDDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
DB 121 FYRKTGLVGFQDMCVPCGDDPPPPYEPHCASKVNLVKISSTVSSPRDTALAAVICSALAT 180

QY 181 VLLALLILCVYCKQFMEKPSWLSRSDIQYNGSELSCLDRLPOLHEYAHRACCCRRD 240
DB 181 VLLALLILCVYCKQFMEKPSWLSRSDIQYNGSELSCFDQPRLRHCAHRAACCCYHRD 240
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Db 181 VLLALLILCVYCKRQFMKKPSKLP 208

RESULT 7

Q9JLL2 PRELIMINARY; PRT; 150 AA.

AC Q9JLL2; (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE TAJ-BETAL.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;

RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,

RT Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-

RT Independent Cell Death.";

RL J. Biol. Chem. 275:15336-15342(2000).

DR EMBL: AF167554; AAF1827.1; -.

SQ SEQUENCE 150 AA; 16728 MW; 4A1B2E93ABEF7FF43 CRC64;

Query Match 32.2%; Score 725; DB 11; Length 150;

Best Local Similarity 82.6%; Pred. No. 1.2e-59;

Matches 123; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

QY 1 MALKVLLEQEKTFETLLVLGLYLSKVTCTGDCRQEQFRDRSGNCVPCNQCGPMELSK 60

Db 1 MALKVLPLHRTVLFATLLFLHLACKVSCETGDCRQEQFRDRSGNCVLCQCGPMELSK 60

QY 61 ECGFGGEGDAQCVTCRLHRFKEDWGQKCPCLDCAVVNRFOKANCSDATCGDCLPG 120

Db 61 ECGFGGEGDAQCVPCPHRFKEDWGQKCPCADLVNRFORANGSHTSDAYCGDCLPG 120

QY 121 FYRKTLLGVFQDMCEVPCGPPPPYEPHC 149

Db 121 FYRKTLLGVFQDMCEVPCGPPPPYEPHC 149

RESULT 8

Q9R187 PRELIMINARY; PRT; 448 AA.

AC Q9R187; (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE ECTODERMAL DYSPLASIA RECEPTOR.

GN EDAR OR DL.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99364417; PubMed=10431242;

RA Headon D.J., Overbeek P.A.;

RT "Involvement of a novel Tnf receptor homologue in hair follicle

RT Induction.";

RL Nat. Genet. 22:370-374(1999).

DR EMBL: AF160502; AAD50425.1; -.

DR MGD; MGI:1343498; Edar.

KW Receptor.

SQ SEQUENCE 448 AA; 48434 MW; FCCAF38F3D6BB971 CRC64;

Query Match 8.7%; Score 197; DB 11; Length 448;

Best Local Similarity 28.2%; Pred. No. 3.6e-10;

Matches 61; Conservative 32; Mismatches 83; Indels 40; Gaps 11;

QY 16 LVLVLLGLYLSKVTCTGDCRQEQFRDR-SGNCVPCNQCGPMELSKGCGFG-YGEDAQCV 73

Db 13 LPVLVVLMSAKAEDSNGENEYHNQTTGLCQCCPPCRGPEPYMSCGVTGKDDYGCV 72

QY 74 TCRHFRFKEDWGQKCPCLDCAVVNRFOKANC-----SATSDAICGDCPLPGFY----RKT 125

Db 73 PCPAERKFSKG-GYQICRRHKDC---EGFFRATVLTTPGDMENDAECCGCPPLGYMLNRRP 128

QY 126 KLGVFQDMCEVPCGPPPPYEPHCASKVNLVKIATSTASSPRDTA-----L 170

Db 129 NIYG---WVCYSC-LLAPPNTKECVGATSGVSAHSTSGGSLSPFQHAHKELSCQGH 184

QY 171 AAVICSALATVL---LALLILCVYCKRQFMKKPS 203

Db 185 ATALIITAMSTIFIMTAIVLIIMFY---IMKTGPS 216

RESULT 9

Q9UNE0 PRELIMINARY; PRT; 448 AA.

AC Q9UNE0; (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)

DE ECTODYSPLASIN-A RECEPTOR PROTEIN.

GN EDAR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99364416; PubMed=10431241;

RA Montreal A.W., Ferguson B.M., Headon D.J., Street S.L., Overbeek P.A.,

RA Zonana J.;

RT "Mutations in the human homologue of mouse dl cause autosomal

RT recessive and dominant hypohidrotic ectodermal dysplasia.";

RL Nat. Genet. 22:366-369(1999).

DR EMBL: AF130988; AAD50076.1; -.

KW Receptor.

SQ SEQUENCE 448 AA; 48582 MW; AC8D61249D608439 CRC64;

Query Match 8.5%; Score 191; DB 4; Length 448;

Best Local Similarity 28.7%; Pred. No. 1.3e-09;

Matches 62; Conservative 30; Mismatches 84; Indels 40; Gaps 12;

QY 16 LVLVLLGLYLSKVTCTGDCRQEQFRDR-SGNCVPCNQCGPMELSKGCGFG-YGEDAQCV 73

Db 13 LPVLVVLMSAKAEDSNGENEYHNQTTGLCQCCPPCRGPEPYMSCGVTGKDEYGCV 72

QY 74 TCRHFRFKEDWGQKCPCLDCAVVNRFOKANC-----SATSDAICGDCPLPGFY----RKT 125

Db 73 PCPAERKFSKG-GYQICRRHKDC---EGFFRATVLTTPGDMENDAECCGCPPLGYMLNRRP 128

QY 126 KLGVFQDMCEVPCGPPPPYEPHCASKVNLVKI-----ASTASSPRDTA-----L 170

Db 129 NIYG---WVCYSC-LLAPPNTKECVGATSGASANFFGTSGSLSPFQHAHKELSCQGH 184

QY 171 AAVICSALATVL---LALLILCVYCKRQFMKKPS 203

Db 185 ATALIITAMSTIFIMTAIVLIIMFY---ILKTGPS 216

RESULT 10

Q9UND9 PRELIMINARY; PRT; 448 AA.

AC Q9UND9; (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)

DE ECTODYSPLASIN-A RECEPTOR PROTEIN.

GN EDAR.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99364416; PubMed=10431241;
RA Monreal A.W., Ferguson B.M., Headon D.J., Street S.L., Overbeek P.A.,
RA Zonana J.;
RT "Mutations in the human homologue of mouse dl cause autosomal
RT recessive and dominant hypohidrotic ectodermal dysplasia.";
RL Nat. Genet. 22:366-369(1999).
DR EMBL; AF130996; AAD50077.1; -.
DR EMBL; AF130990; AAD50077.1; JOINED.
DR EMBL; AF130991; AAD50077.1; JOINED.
DR EMBL; AF130992; AAD50077.1; JOINED.
DR EMBL; AF130993; AAD50077.1; JOINED.
DR EMBL; AF130994; AAD50077.1; JOINED.
DR EMBL; AF130995; AAD50077.1; JOINED.
KW Receptor.
SQ SEQUENCE 448 AA; 48572 MW; AC8F80F79CB255EA CRC64;

Query Match 8.5%; Score 191; DB 4; Length 448;
Best Local Similarity 28.7%; Pred. No. 1.3e-09;
Matches 62; Conservative 30; Mismatches 84; Indels 40; Gaps 12;

QY 16 LVLVLLGYLSKVTCTGDCRQOEFRRD-SGNCVPCNOCGPGMELSKGFG-YGEDAOCV 73
DB 13 LPLVVLVSLMCSARAYSNGENEYNYQTGLCQECPCPGGEEPYLSGCGYTKDEDYGCV 72

QY 74 TCLRHRFKEDMGFKCKPCLDCAVNNRFQKANC-----SATSDAICGDCLPGFY-----RKT 125
DB 73 PCPAEKFSKG-GYQICRRHKDC---EGFRATVLPFGDMENDAEAGCPCLPGYMYLENRPR 128

QY 126 KLIVGFQDMECVCPGDPDPPEYEPHCASKNLVKI-----ASTASSPRDTA-----L 170
DB 129 NIYG---MVCYSC-LAPNTKECVGATSGASANFPGTSGSSTLSPFQHAHKLMSGOGHL 184

QY 171 AAVICSALATVL---LALLILCVICKRQFMKKPS 203
DB 185 ATALLIAMSTFIIMAIIVLIIMFY-----ILATKPS 216

RESULT 11
Q9PVD4 PRELIMINARY; PRT; 387 AA.
AC Q9PVD4;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)
DE P75-LIKE TRANSMEMBRANE PROTEIN FULLBACK.
OS Xenopus laevis (African clawed frog)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Hick E., Sun B.I., Collins-Racie L., LaVallie E., Sive H.L.;
RT "Identification and Characterization of fullback, a Novel Posteriorly-
RT Expressed Xenopus Gene.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF131890; AAD54072.1; -.
DR HSP; P07174; INCR.
DR INTERPRO; IPR000488; -.
DR INTERPRO; IPR001368; -.
DR PFAM; PF00020; TNFR_c6; 4.
DR PFAM; PF00531; death; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_3.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
KW Transmembrane.

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SQ SEQUENCE 387 AA; 42066 MW; 1A386A239C7C8A82 CRC64;

Query Match 7.6%; Score 170.5; DB 13; Length 387;
Best Local Similarity 23.6%; Pred. No. 8.7e-08;
Matches 69; Conservative 35; Mismatches 93; Indels 95; Gaps 15;

QY 16 LVLVLLGYLSKVTCTGDCRQOEFRRD-SGNCVPCNOCGPGMELSKGFGYGEDAQCVC 75
DB 12 LLLLSKISAEDVCESG-----LYTNSGKC--CSLCPAGFGVVVPCG---DSDTKCEPC 60

QY 76 RLHRPKEDMGFQ-----KCKPCLDCAVNNRFQKANCATSDAIC-----GDC 117
DB 61 -----IENSTFSDVRSAAKAKQPCFTCQSPSLTLESNCTREQDTVCRCPERGYLDSNGIC 115

QY 118 LP-----GFYRKTKLVGFQDMECVPC-----G 139
DB 116 LPCQLCSKGGHVVSOCTHKNNTVQLCSGGFYSEVK-----SSESPCLPCRCKTEKETEVOIG 172

QY 140 DPPPPEYEPHCASK-VNLVK-----IASTASS-----PRDTA--LAAVICSALATVLLALL 186
DB 173 DCVPQHDILCDKQVPIPKRTGEGENGTSAGSPHPIPDQNSKNIIPVYCSILAAVVVGLI 232

QY 187 ILCVYICKRQFMKKPSWLSRSDI--QYNGSELS-----CLDRPOLHEYAH 231
DB 233 AYVAFKCYTCTCKQKKQAKARAGELATSTEGEKLHNDSGVFLDTHSLOEPNH 284

RESULT 12
Q9N092 PRELIMINARY; PRT; 430 AA.
ID Q9N092;
AC Q9N092;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)
DE UNNAMED PORTEIN PRODUCT.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain CDNA
RT libraries.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB046039; BAB01621.1; -.
SQ SEQUENCE 430 AA; 45850 MW; BA8DE92593E1E859 CRC64;

Query Match 6.4%; Score 144.5; DB 6; Length 430;
Best Local Similarity 21.3%; Pred. No. 2.5e-05;
Matches 57; Conservative 29; Mismatches 83; Indels 99; Gaps 8;

QY 51 QCGPGMELSKGCGYGEDAQCVCVTCRLHRFKEDMGFKCKPCLDCAVNNRFQKANCATS 110
DB 31 QCGPG-----EEDPLNPGOGTLCRPPPGTFSAAWSSSCQPHARCSLQRLAQAQVATQ 86

QY 111 DAICGDCPLPGFYRKTKLVGFQDMECVCPGDPDPPEYEPHCASKNL-----VK 157
DB 87 DTLCGDCWPGWFG-----PWGVPVPCQPCSWAPLGIHGCDGEMRRARRGVE 133

QY 158 IASTASS-----PRDTALA-AVICASALATVLLALLILCVYICKRQFMKK 201
DB 134 VAAAGASSGGETRQPGNGTRAGGPEETAQAQYAVI--AIVPVFCLMGLLGLVLC----- 183

QY 202 PSWLSRSDIQYNGSELSCLDRPOLHEYAHRAACCCCRDRSVQTCGVRLLPSMCCEACS 261
DB 184 -----NLLKRGYHCTAHK-----EVG 200

QY 262 PNPATIGCGVHSAASLIQARNAGPAGEMV 289

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Db 201 PGPGGGGGINPAYRTEDVNEGTIGLV 228

RESULT 13

Q9Z0W1 PRELIMINARY; PRT; 417 AA.
AC Q9Z0W1; 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE NERVE GROWTH FACTOR RECEPTOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A;
RX MEDLINE=99077793; PubMed=9857182;
RA Tuffreau C., Benjean J., Blondel D., Kieffer B., Flament A.;
RT "Low-affinity nerve-growth factor receptor (p75NTR) can serve as a
RT receptor for rabies virus";
RL EMBO J. 17:7250-7259(1998).
DR EMBL; AF105292; AAD17943.1; -.
DR HSSP; P07174; INGR.
DR INTERPRO; IPR000488; -.
DR INTERPRO; IPR000561; -.
DR INTERPRO; IPR000734; -.
DR INTERPRO; IPR001368; -.
DR PFAM; PF00020; TNFR_6; 4.
DR PROSITE; PS00452; TNFR_NGFR_1; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
KW Receptor.
SQ SEQUENCE 417 AA; 44686 MW; 5D7A4510DB8AF9B2 CRC64;

Query Match 6.3%; Score 142; DB 11; Length 417;
Best Local Similarity 22.4%; Pred. No. 4.2e-05;
Matches 93; Conservative 50; Mismatches 178; Indels 94; Gaps 23;

QY 7 LEQETFTLLVLLG--YLCKVTCTGDCRQOEFDRSGNCVPCNQCGMELSKCGF 64
Db 1 MDRLLLLLLLLLVGSGAKETCTG-----MYTHSGEC--CKACNLGEGVAQPCG- 51
QY 65 GYGEDACQVTCRLHREKED--WGFOCKPCLDCAVNVRFQKNCATSDAICGDCPLPGFY 122
Db 52 --ANQTVCEPCLDSTVTFSDVVSATEPCCKTECLGL-QSMAPCVADDAVC-RCSYGY 107
QY 123 RYTKLVGFQDME-----CVPCGDPPPPYEPHCASKNVLV-----KIATASSPRDTAL 170
Db 108 -----QDEETGRCEACSVCG-VGSLGVFSCDQKNTVCECPGTYSDANHVDPCL 158
QY 171 AAVICSAATVLLALLILCVYCKRFMEKKPSWSLSRSDIQNGSELCLDRPQLHEYA 230
Db 159 PCTVCEDTERQLRE----CTPWADAEEETIPGRWITRSTPPE--GSDVT---TPSTQE-- 207
QY 231 HRACCCCRDRSVOTCGPVR-LLPMSMCEEACSPNATLPGCVHSAASLQARNAGPAGEMV 289
Db 208 -----PEAPPERDLIASTVAD-----TVITVMGSSQPVVTR--GTADNLI 245
QY 290 PTFPGSLTSGICEFS-----DAMPLQNPMPGGDNISFCDSYBELTGEDTHSLNPELESST 345
Db 246 PIVYCSLLAAVVGVLVYIAFKRNWSCONKQGNRSRPNQTPPEGEKLSH-----DSGI 300
QY 346 SLDSNSQDLVGVAVPQSHSENFATDLSRYNNLTVESASTQDALTWRSLDQ 400
Db 301 SVDSQSLHD-----QQHTQT--TASAQALKGDNLYSSL-----PLTKREEVEK 342

RESULT 14

O14865 PRELIMINARY; PRT; 426 AA.
AC O14865;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE DEATH RECEPTOR 3 BETA.
GN DR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98113360; PubMed=9446802;
RA Warzocha K., Ribeiro P., Charlot C., Renard N., Coiffier B.,
RA Salles G.;
RT "A new death receptor 3 isoform: expression in human lymphoid cell
RT lines and non-Hodgkin's lymphomas";
RL Biochem. Biophys. Res. Commun. 242:376-379(1998).
DR EMBL; AF026070; AAC39556.1; -.
DR HSSP; P19438; INCF.
DR INTERPRO; IPR000488; -.
DR INTERPRO; IPR000561; -.
DR INTERPRO; IPR001368; -.
DR PFAM; PF00020; TNFR_6; 2.
DR PFAM; PF00531; death; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ SEQUENCE 426 AA; 45950 MW; 371AA7F16AD29C16 CRC64;

Query Match 6.3%; Score 142; DB 4; Length 426;
Best Local Similarity 25.2%; Pred. No. 4.3e-05;

Matches 66; Conservative 26; Mismatches 70; Indels 100; Gaps 14;

QY 34 CRQOEFDRSGNC--VPCNQCG--PMELSKCGFGYGEDACQVTCRLHREKEDWGFGKC 89
Db 95 CDEQASQVALENCASVADTRCGCKPGFV--EC-----QVSQCVSPPF-----YC 138
QY 90 KPCLDCAVNVRFQKNCATSDAICGDCPLPGFYRKTKLVGFQDMECVPCGDPPPPYEPHC 149
Db 139 QPCLDCAVNVRFQKNCATSDAICGDCPLPGFYRKTKLVGFQDMECVPCGDPPPPYEPHC 184
QY 150 ASKVNVLKIASTASSPRDTALAAVICSAL-----ATVLLALLILCVYCKRQPMERK 201
Db 185 -----SLAGAPWAGVQSAVPLSVAGGRVGVFWQVLLAGLVVPLL----- 225
QY 202 PSWSLSRSDIQNGSELCLDRPQLHEYAHRAACCCQCRDRSVOTCGPVRLLPSMCCE----- 257
Db 226 -----GATLT-----YTYRH-----CWPBK--PLVTADAEAGM 250
QY 258 EACSPNATLPGCVHSAASLQA 279
Db 251 EALTTPPPATHLPLDSATLLA 272

RESULT 15

O72735 PRELIMINARY; PRT; 186 AA.
AC O72735;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE A53R PROTEIN.
GN A53R.
OS Cowpox virus (CPV).
OC Viruses; GSDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.

```
OX NCBI_TaxID-10243;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-GRI-90;
RX MEDLINE-98229462; PubMed-9568042;
RA Shchelkunov S.N., Saifonov P.F., Totmenin A.V., Petrov N.A.,
RA Ryazankina O.I., Gutorov V.V., Kotwal G.J.;
RT "The genomic sequence analysis of the left and right species-specific
RT terminal region of a cowpox virus strain reveals unique sequences and
RT a cluster of intact ORFs for immunomodulatory and host range
RT proteins.";
RL Virology 243:432-460(1998).
DR EMBL; Y15035; CAA75273.1; -.
DR HSSP; P25942; ICDF.
DR INTERPRO; IPR001368; -.
DR PFAM; PF00020; TNFR_C6; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
DR PRODOM; PD000771; -. 1.
SQ SEQUENCE 186 AA; 20482 MW; D2342F1040A00AE3 CRC64;

Query Match          6.1%; Score 137.5; DB 12; Length 186;
Best Local Similarity 28.0%; Pred. No. 4.4e-05;
Matches 46; Conservative 18; Mismatches 69; Indels 31; Gaps 11;

QY 11 KTFFTLLVLLGYLSCKVTCE-----TGDCRQDEFDRDRSGN-CVPCNQCGPGMEL 58
   | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 4 KSLAVACVIL-YITTLVTADIPTPLPPHAPVNGSCDEGEYLDKRHNQC--CNQCPGGEFA 60

QY 59 SKECGFGYGED-AQCVCRLHREKEDMGFQK-CKPCLDCAVVNRFOKANCATSATSDAICGD 116
   | | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db 61 KVRCS---GSDNTKGERCPHTYTAIPNYSNGCHQCRKCP-TGSFQKVKCTGTQNSKC-S 115

QY 117 CLPGFYRKTKLVGFQD-MECVPCGDPPEPY-----EPHCAS 151
   | | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db 116 CLPGWICATDSSQTECDRCDCVPKRCPCGYFGIDEQGNPICKS 159

Search completed: February 16, 2001, 21:09:00
Job time: 235 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 01:56:55 ; Search time 4027.99 Seconds
(without alignments)
2207.677 Million cell updates/sec

Title: us-09-380-276A-1
Perfect score: 1269
Sequence: 1 atggcttaaaagtgtact.....ggcagcagctgggtccctg 1269

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues
Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	302.2	23.8	395	106	BE306459	BE306459 601103459
2	296.4	23.4	454	147	W56629	W56629 xdl6e11.r1
3	274.8	21.7	282	28	AL036000	AL036000 DKFZp564K
4	241.2	19.0	534	135	BE57704	BE57704 212225 MA
5	203	16.0	401	1	AA003356	AA003356 mg49q01.r
6	192.8	15.2	369	91	AA03356	AA03356 mg49q01.r
7	174.8	13.8	358	1	AA036247	AA036247 ml74a03.r
8	157.6	12.4	258	133	BB542020	BB542020 BB542020
9	155	12.2	643	159	AQ563354	AQ563354 HS_5335_B
10	125.8	9.9	646	159	AQ544065	AQ544065 RPCI-11-3
11	124.4	9.8	275	31	AV111112	AV111112 AV111112
12	120.8	9.5	404	8	AA495217	AA495217 fa04g10.r
13	113.8	9.0	450	158	AQ514075	AQ514075 HS_5184_A
14	95	7.5	1110	193	CNS0507C	AL347097 Tetraodon
15	91.2	7.2	414	91	AW527025	AW527025 UI-R-B01-
16	80.2	6.3	381	21	AI551729	AI551729 vfl1e02.y
17	67.4	5.3	442	109	BE554624	BE554624 ur48c11.y
18	59	4.6	405	150	AQ173919	AQ173919 HS_3204_A
19	42.6	3.4	443	11	AA759377	AA759377 ah54a10.s
20	41.4	3.3	551	12	AA814296	AA814296 nz07d08.s
21	39.4	3.1	397	13	AA860208	AA860208 ak48c10.s
22	39.4	3.1	266	128	BB350382	BB350382 BB350382
23	39.2	3.1	266	128	BB350382	BB350382 BB350382
24	39	3.1	407	146	W32428	W32428 zc05c12.s1
25	39	3.1	559	3	AA161105	AA161105 z058c05.s
26	38.8	3.1	706	109	BE535395	BE535395 601103459
27	38.8	3.1	925	190	CNS0091P	AL053013 Drosophila
28	38	3.0	391	21	AI522266	AI522266 t184f06.x
29	38	3.0	597	97	AW968349	AW968349 EST380424
30	37.8	3.0	458	88	AW303441	AW303441 xv19b01.x
31	37.8	3.0	482	139	BF018062	BF018062 ur95a06.x
32	37.6	3.0	510	29	AU060928	AU060928 AU060928
33	37.4	2.9	319	103	BB219800	BB219800 BB219800
34	37.4	2.9	343	96	AW877284	AW877284 MR4-PT005
35	37.4	2.9	472	7	AA417295	AA417295 zu18c03.s
36	37.4	2.9	968	193	CNS056T4	AL323761 Tetraodon
37	37.4	2.9	1002	191	CNS0206F	AL208896 Tetraodon
38	37.2	2.9	344	37	AV630854	AV630854 AV630854
39	37.2	2.9	372	89	AW312781	AW312781 5078 MARC
40	37	2.9	910	190	CNS0060N	AL065629 Drosophila
41	36.8	2.9	366	8	AA542636	AA542636 fa08d10.r
42	36.8	2.9	447	17	AI217695	AI217695 qh26d07.x
43	36.8	2.9	465	38	AW015051	AW015051 UI-H-B10-
44	36.8	2.9	465	87	AW181919	AW181919 xj68d07.x
45	36.8	2.9	689	109	BE532858	BE532858 601234740

ALIGNMENTS

RESULT 1

BE306459

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

BE306459 395 bp mRNA
 601103459F1 NCI_CGAP_Lu29 Mus musculus cdna clone IMAGE:3495566 5',
 mRNA sequence.
 BE306459
 BE306459.1 GI:9159707
 EST.
 house mouse.

13-JUL-2000
 EST
 IMAGE:3495566 5',

ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 395)
TITLE	NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/ .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM8546 row: f column: 15 High quality sequence stop: 395. Location/Qualifiers 1..395
FEATURES	source

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Stem cell origin."
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
88 a 101 c 120 g 86 t
BASE COUNT
ORIGIN
Query Match 23.88; Score 302.2; DB 106; Length 395;
Best Local Similarity 85.3%; Pred. No. 2.8e-78;
Matches 337; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

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	Qy	56	tactaggctattgtcatgtaaaagtgacttgtgaacacaggagactgtagacagaagaat	115
	Db	1	TCTACTACCCACTTTGGCATGTAAAGTGAATTGCGAATCCGGAGATTGCAGGCAGGAAT	60
	Qy	116	tcagggaatcgctcggaaaacttgtttccctgcacaaccagtgtgggcccaaggcatgagattgt	175
	Db	61	TCAAGGATCGATCTGGAAAACCTGTCTCTCTCAAACAGTCGGACCTGGCATGGAGTTGT	120
	Qy	176	ctaagggaatgtggcttcggtctatgggagagatcacagtgtgtgacgtgccgcggtgcaca	235
	Db	121	CCAAGGAATGTGGCTTCGGCTATGGGAGGATGCACAGTGTCGCCCTGCAGGCCGCACC	180
	Qy	236	ggttcaaggagactggggcttcagaaaaatcaagccctgtctggaactgcgcagtgtga	295
	Db	181	GGTTCAAGGAAGACTGGGGTTTTCCAGAAGTGTAAAGCCGTGTGCGGACTGTGCGCTGGTGA	240
	Qy	296	acgcctttcagaaggcaaatgtgttcagcccccaadtgatcccatctgsggggactgcttgc	355
	Db	241	ACCGCTTTTCAGAGGGCCCAACTGCTCACACACCAGTGATGCTGTGCGGGGACTGCCCTGC	300
	Qy	356	caggatatttaggaagacgaacctgttcggctttcaagacatgagttgtgtgctctgtg	415
	Db	301	CAGGATTTTACCGGAAGCAACAACCTGGTTGGTTTTCAAGACATGGAGTGTGTGCCCTGCG	360
	Qy	416	gagacctctctctcttaaagaaocgcactgtgccc	450
	Db	361	GAGACCCACCTCCTCCTTACGAACCACTGCTACC	395

RESULT	2	W56629	454 bp	mrna	EST
W56629					
LOCUS					

zdl6ell.r1 Soares_fetal_heart_NBHH19W Homo sapiens cDNA clone
 IMAGE:340844 5', mRNA sequence.
 W56629
 VERSION
 KEYWORDS
 EST.
 human.
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 (bases 1 to 454)
 AUTHORS
 Hillier,L.M., Clark,N., Kucaba,T., Le,M., Lennon,G., Warra,M., Parsons,J.,
 M., Hultman,M., Dubuque,T., Elliston,K., Hawkins,M., Holman
 Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
 ,R., Williamson,A., Wohldmann,P. and Willson,R.
 The WashU-Merck EST Project
 Unpublished (1995)
 CONTACT: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL: contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1373 Std Error: 0.00
 Seq primer: mob.REGA+ET.
 FEATURES
 Location/Qualifiers
 1..454
 /organism="Homo sapiens"
 /db_xref="GDB:1266219"
 /db_xref="taxon:9606"
 /clone="IMAGE:340844"
 /clone_lib="Soares_fetal_heart_NBHH19W"
 /sex="unknown"
 /dev_stage="19 weeks"
 /lab_host="DH10B (ampicillin resistant)"
 /notes="Organ: heart; Vector: pT7T3D (Pharmacia) with a
 modified polylinker; Site:1: Not I; Site:2: Eco RI; 1st
 strand cDNA was primed with a Not I oligo(dT) primer [5'
 TGTTCACATCTGAAGTCGAGCGGCATCTTTTCTTTTTTTTTTTT 3']
 double-stranded cDNA was size selected, ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT7T3 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by
 M.Fatima Bonaldo. This library was constructed from the
 same fetus as the fetal lung library, Soares fetal lung
 NBHL19W."
 132 a 96 c 88 g 138 t
 BASE COUNT
 ORIGIN

	Query Match	23.4%	Score 296.4	DB 147	Length 454
	Best Local Similarity	99.7%	Pred. No. 1.5e-76		
	Matches 297	Conservative 0	Mismatches 1	Indels 0	Gaps 0
Qy 972	ctcttaccctgaacctactggaagaacattctctcaatccagaacctgaagagctc	1031			
	1 CTCTATTCCGAACTCACTGGAGNAGACATTCTCTCAATCCAGAACTTGAAGCTC	60			
Db					
Qy 1032	aacgtctctttggattccaataatgacgagctcaagatttggttgggtggggctgtttccagttccagctc	1091			
	61 AACGTCCTTTGGATTCAAAATAGCAGTCGAAGATTTTGGTTGGTGGGGCTGTCTTCAGTCCAGTC	120			
Db					
Qy 1092	tcattctgaaacactttacagcagctactgattctatctagatataaacaacacactgggtaga	1151			
	121 TCATTCTGAAAACCTTTACAGCAGCTACTGATTTATCTAGATATAACAACACACTGGTAGA	180			
Db					
Qy 1152	atcagctaaactcaagatgcactaactatgagaagccagctagatcagagagagtggcgc	1211			
	181 ATCAGCATCAACTCAGAGATGCATTAACATATGAGAAGCCAGCTAGATCAGGAGAGTGGCGC	240			
Db					
Qy 1212	tatcatccaccagccactcagacgtcctctccaggttaagcacacgactagagttccctga	1269			

EST 15-OCT-1996

Db 241 TGTGATCCAGCCAGCTCAGAGTCCCTCCAGGTAAAGCAGGACTGGTTCCTCG 298
|||||
RESULT 3
AL036000 282 bp mRNA EST 29-FEB-2000
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AL036000 282 bp mRNA EST 29-FEB-2000
DKFZ564K1022.r1 564 (synonym: hfbr2) Homo sapiens cDNA clone
DKFZ564K1022 5', mRNA sequence.
AL036000
AL036000:1 GI:5405629
EST.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 282)
Wambutt.R., Heubner.D., Mewes.H.W., Gassenhuber.J. and Wiemann,S.
EST (Wambutt, et al.)
Unpublished (1999)
Contact: Wambutt R
MIPS
Am Klopferstr. 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
SI sequence also available.
This clone (DKFZ564K1022) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source
1..282
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZ564K1022"
/clone_lib="564 (synonym: hfbr2)"
/tissue_type="brain"
/dev_stage="fetal"
/lab_host="Xl-2blue"
/note="Vector: pAMPl; Site_1: NotI; Site_2: SalI"
BASE COUNT 57 a 85 c 75 g 63 t
ORIGIN

Query Match 21.7%; Score 274.8; DB 28; Length 282;
Best Local Similarity 98.6%; Pred. No. 3.1e-70;
Matches 276; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 365 ataggagagaaactgtcggtttcaagacatggagtgtgcttgcctgtggagaccctc 424
Db 3 ATAGGAAGAGAAACTTGTGGCTTTCAAGACATGGAGTGTGGCTTGTGGAGCCCTC 62
QY 425 ctctctctacgaaccgactgtgccagcaaggtccaacctcgtgaagatcgcgctccacgg 484
Db 63 CTCTCTCTACGAACCGCACTGTGCCAGCAAGGTCAACCTCGTAGAGATCGCTCCACGG 122
QY 485 cctccagccacgggacacggcgctgctgtatctatctcagcgctctgcccacgctcc 544
Db 123 CCTCAGCCACGGGACACGGCGCTGGCTGCCGTATCTGCANCGCTCTGGCCACCGTCC 182
QY 545 tgcctggcctgctcatcctctgctcatctattgtaagacagatttatgagaagaac 604
Db 183 TGCTGGCCCTTGCTCATCTCTCTGTGTATCTATTGTATAGACAGACTTTATGGAGAANAAC 242
QY 605 ccagctggtctctgctgctcagagacattccagtacaacgg 644
Db 243 CCAGCTGGTCTCTGCGGTGCGCANGACATTCAGTACTACGG 282

RESULT 4
BE757704

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BE757704 534 bp mRNA EST 15-SEP-2000
212225 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
BE757704
BE757704.1 GI:10171696
EST.
COW.
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 534)
Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
W.W. and Keele,J.W.
Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGAAACAGCTATGACCAT
BACKWARD: GTTTCACGTCAGCAGC
Plate: 65 row: C column: 2
Seq primer: ATTGAGTGACACTATAG.
FEATURES
source
1..534
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from testis, thymus,
semilendonsus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
BASE COUNT 122 a 117 c 171 g 124 t
ORIGIN

Query Match 19.0%; Score 241.2; DB 135; Length 534;
Best Local Similarity 83.6%; Pred. No. 3.4e-60;
Matches 286; Conservative 0; Mismatches 53; Indels 3; Gaps 1;
QY 1 atggctttaaagtctactagaacaagagaaaacgtttttcactcttttagtattacta 60
Db 196 ATGGCTTCAACGTGCTACTCAGGCAACAGAAA---TCCTTCACGGTTGTGTTTACTA 252
QY 61 ggctattgtctgaagtgtactgtgaaacaggagactgtgacagcaagaattcagg 120
Db 253 GCCTGTTTGGCATGTGGAGTGATTGTGAAACAGGAGACTGTGACAGCAGGAATTACAG 312
QY 121 gatcggtctggaactgtgtccctcgcaaccagtgtg9ccagggcatgaggtgtctaa 180
Db 313 GACCAGTCAGAGAGCTGTGTCTGTGCAAGCAGTGTGGCCAGGCATGGAGTTGTCCAAG 372
QY 181 gaatggcttcggctatgggagagatgcacagtgtgacgtccggctgcacaggttc 240
Db 373 GAATGTGGCTTTGGCTACGGGGGAGGAGCCCGCAGTGTGTGAAGTGGCCGCCACAGGTT 432
QY 241 aaggaggactggggtctccagaaatgcaggccctgtctgactgcgagtggtgaaccgc 300
Db 433 AAGGAGGACTGGGCTCTCAGAAAGTCAACGCGTGGCTGGACTGCGCCCTGCTGAGCCGC 492
QY 301 ttccagaagcaaatgttccagccaccagtgtgccaatctgc 342
Db 493 TTCCAGAAGCCCAACTGCTCGGCCACTTGGCGCAGCGCGCTCTGC 534

```
RESULT 5
AA003356 401 bp mRNA EST 19-JUL-1996
LOCUS mg49g01.r1 Soares mouse embryo NBME13.5 14.5 Mus musculus cDNA
DEFINITION clone IMAGE:427152 5', mRNA sequence.
ACCESSION AA003356
VERSION AA003356.1 GI:1446796
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 401)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:261704
Seq primer: ETPRimer
High quality sequence stop: 345.
FEATURES
source
Location/Qualifiers
1..401
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:427152"
/clone_lib="Soares mouse embryo NBME13.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/note="vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGGAGCGCGGAAATTTTTTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT73 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo."
BASE COUNT 92 a 96 c 128 g 85 t
ORIGIN
Query Match 16.0%; Score 203; DB 1; Length 401;
Best Local Similarity 78.8%; Pred. No. 6e-49;
Matches 242; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
QY 1 atggctttaaagtgctactagaagaagaaagctttttcactcttttagtatacta 60
DB 95 ATGGCACTCAAGGTCTTACTCTACACAGGACGGTGCTCTTCGCTGCCATTTCTCTCTA 154
QY 61 ggcatttgtcattgaagtactgtgaacacagagagactgtagacagcaagaattcagg 120
DB 155 CTCACCTGGCATTGAAGTGAAGTTCGGAACCGGAGATTGAGGAGCAGGAAATTCAG 214
```

```
QY 121 gatcggctctggaacctgtgttccctgcaaccagtggtggccaggcatggagtgtcttaag 180
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 215 GATCGATCTGGAAACTGTGTCTCTGCAACAGTGGCGACCTGGCATGGAGTTGTCGAAG 274
QY 181 gaatgtgcttcggctatgggagagatgcacagtgctgtgacgtgcggctgcacaggttc 240
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 275 GAATGTGCTTCGGCTATGGGAGGATGCACAGTGTGTGCCCTGCAGCGCCGACCGGTTTC 334
QY 241 aaggaggactgggctccagaaaatgcaagccctctctggactgcgcagtggtgaaccgc 300
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 335 AAGGAAGACTGGGGTTTCCAGAAGTGTAAAGCATGTGCGGACTGTGCGCTGGTGAACCGC 394
QY 301 ttccaga 307
|||||
DB 395 TGTCCAGA 401
RESULT 6
AA478317 369 bp mRNA EST 07-JUL-2000
LOCUS AW478317
DEFINITION 19558 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION AW478317
VERSION AW478317.1 GI:7048423
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 369)
Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M.,
Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Laegreid
,W.W. and Keeler, J.W.
Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCCAGTCACGACG
Plate: 10 row: M column: 8
Seq primer: ATTTAGGTGACACTATAG.
FEATURES
Location/Qualifiers
source
1..369
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from testis, thymus,
semitendinosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
BASE COUNT 60 a 115 c 115 g 79 t
ORIGIN
Query Match 15.2%; Score 192.8; DB 91; Length 369;
Best Local Similarity 72.9%; Pred. No. 6.1e-46;
Matches 248; Conservative 0; Mismatches 92; Indels 0; Gaps 0;
QY 736 gggcgggtgcgttctccatccatgctgtgaggagcctgcagcccccaaccggcg 795
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 26 GGGCCAGTCACCTTGTCCCTCCCGGTGCTGTGTGGGGCTGCGGCATTGCGCCGGGAC 85
```


Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES

Location/Qualifiers
source

1. .258
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="E130118G08"
/clone_lib="RIKEN full-length enriched, 0 day neonate eyeball"
/tissue_type="eyeball"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
GAGAGAGAGCGGCCCAACTCGAGTTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
GAGAGAGATTCGAGTAAATTAATCCCGCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
BASE COUNT 55 a 77 c 66 g 60 t
ORIGIN

Query Match 12.4%; Score 157.6; DB 133; Length 258;

Best Local Similarity 80.7%; Pred. No. 1.4e-35;
Matches 184; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 221 cgtccgctcacaggttcagagagactgggcttcagaaatgcagccctgtctgg 280
Db 1 CTGAGCGCCCGCCGGTCTAAGAAGACTGGGCTTCCAGAAGTGAAGCCATGTGGCG 60
Qy 281 actgcagtggtgaaccgcttcagagagcaaatgttcagccaccagtgatgcacat 340
Db 61 ACTTTCGCTGTGAACCGCTTTCAGAGGCCCACTGCTCACACCACTGATGCTTTT 120
Qy 341 gcggggactgctgccaggttttatagagacgaaactgtcggtttcaagacatgg 400
Db 121 GCGGGAGTGCCTGCCAGATTTTACCGGAGAGACCAACTGGTGGTTTTCGAAGACATGG 180
Qy 401 agtgtgctctgtggagaccctcctcctctacgaacccactgtg 448
Db 181 AGTGTGCTCCCTGGAGACCCACTCTCCTCCTAGAACACCACTGTG 228

RESULT 9

AQ563354 643 bp DNA GSS 29-MAY-1999
LOCUS HS_5335_B2_B03_87A RPCI-11 Human Male BAC Library Homo sapiens
DEFINITION genomic clone Plate=911 Col=6 Row=D, DNA sequence.
ACCESSION AQ563354
VERSION AQ563354.1 GI:4922825
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 643)
AUTHORS Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D., and Hood, L.

TITLE

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

JOURNAL MEDLINE COMMENT

99380589

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering.bac.htm>)

or from Research Genetics (<http://info@resgen.com>). BAC end Web Server:

<http://www.htsc.washington.edu>

Plate: 911 row: D column: 6

Seq primer: T7

Class: BAC ends

High quality sequence stop: 643.

FEATURES

Location/Qualifiers
source

1. .643

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="Plate=911 Col=6 Row=D"

/clone_lib="RPCI-11 Human Male BAC Library"

/sex="male"

/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;

Male blood DNA was isolated from one randomly chosen donor

and partially digested with a combination of EcoRI and

EcoRI Methylase. Size selected DNA was cloned into the

pBACe3.6 vector at EcoRI sites"

BASE COUNT 151 a 154 c 158 g 167 t 13 others
ORIGIN

Query Match 12.2%; Score 155; DB 159; Length 643;

Best Local Similarity 85.9%; Pred. No. 1.1e-34;

Matches 170; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy 445 tgtgccagcaaggtcaacctcgtgaagatcgctccagccgctccagccacggacacg 504

Db 315 TGTGCCAGCAAGGTCAACCTCGTGAAGATCGGTNCACGGCTCCAGCCACGGGACAGC 374

Qy 505 gcgctggctgcggttatctgcagcgtctggccaccgctcctgctggcctgctatcttc 564

Db 375 GCGCTGTGCTGCCGATCTGCAGCGCTCTGGCCACCGCTCTGCTGCTCATCTC 434

Qy 565 tgtgtcatctattgaagacagatttatggagaagaacccagctggtctctgcggtca 624

Db 435 TGTGTCTCTATTGTAAGAGACAGTNTATGGAGAGAAACCCAGCTGTAAAGTTGAGCT 494

Qy 625 caggacattccagtaaac 642

Db 495 CATTACATNTCTTATCAC 512

RESULT 10

AQ544065 646 bp DNA GSS 19-MAY-1999
LOCUS RPCI-11-315F10.TV RPCI-11 Homo sapiens genomic clone RPCI-11-315F10
DEFINITION , DNA sequence.
ACCESSION AQ544065
VERSION AQ544065.1 GI:4869459
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 646)
AUTHORS Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.

TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
JOURNAL Unpublished (1997)
COMMENT Other_GSSs: RPCI-11-315F10.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbest@igf.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@edj.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.

FEATURES
Source

Location/Qualifiers
1. .646
/organism="Homo sapiens"
/db_xref="GDB:7620705"
/db_xref="taxon:9606"
/clone="RPCI-11-315F10"
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"
BASE COUNT 175 a 135 c 145 g 191 t
ORIGIN

Query Match 9.9%; Score 125.8; DB 159; Length 646;
Best Local Similarity 94.9%; Pred. No. 4.8e-26;
Matches 130; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 611 ggtctcgagtcacaggacattcagtaacagcgtctgaagctgctgtcttgacagac 670
|||||
Db 263 GGTCTCGCGTCACAGGACATTCAGTACACGGCTCTGAGCTGCTGTTTGACAGAC 322
QY 671 ctgagctccacgaataatgcccacagagcctgctgccagtgccgcctgactcagtcgaga 730
|||||
Db 323 CTCAGTCCACGAATATGCCACAGAGCCTGCTGCCAGTGCCGCCGTGACTCAGTCAGAC 382
QY 731 cctgcgggcccgggtgcgc 747
|||||
Db 383 CCGTGGGTAAGTTTCAGC 399

RESULT 11
AV111112 275 bp mRNA EST 29-JUN-1999
LOCUS AV111112 Mus musculus C57BL/6J 10-day embryo Mus musculus cdna
clone 2600016N17, mRNA sequence.
ACCESSION AV111112
VERSION AV111112.1 GI:5265192
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 275)
AUTHORS Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tomimaga, N., Watanabe, S., Yagane, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
TITLE RIKEN Mouse ESTs

JOURNAL
COMMENT

Unpublished (1999)
Contact: Chie Owa
Genome Science Laboratory
RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES
Source

Location/Qualifiers
1. .275
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="2600016N17"
/clone_lib="Mus musculus C57BL/6J 10-day embryo"
/sex="mixed"
/dev_stage="10-day embryo"
BASE COUNT 77 a 86 c 55 g 57 t
ORIGIN

Query Match 9.8%; Score 124.4; DB 31; Length 275;
Best Local Similarity 71.3%; Pred. No. 9.1e-26;
Matches 164; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
QY 245 aggaactggggtccagaaatgcaagcctgtctggaactgcagtggtgaacgccttc 304
|||||
Db 43 AGAAAGTGGTTTCCAGAGTAAGAACCCATTGCCCAACCTGCCCTGTAGAACCCCTATC 102
QY 305 aagaagcaaatgttcagccaccagtgatgccatctgcgggactctgtgccaggatttt 364
|||||
Db 103 TGAGGACCCATTCCTCACACACACACTGATGCTCTGCGGGGACTGCCTGCCAAGATTTT 162
QY 365 ataggagcagcaaatgttcgcttcacagacatggagtggtgctgtgagacccctc 424
|||||
Db 163 ACCAGAAAGACCAAACTGGTTGGTTTTCAGACATGAGTGTGTGCCCTCGGAGACCCAC 222
QY 425 ctctcctctacgaaccgcacactgtgccagcaagtcacacctcgtaagatc 474
|||||
Db 223 CTCTCTCCCTACGAAACACACAGTGTGATGTGCCAAGTGGCAGACAGACC 272

RESULT 12

AA495217 404 bp mRNA EST 27-JUN-1997
LOCUS fa04d10.r1 zebrafish ICRFzfls Danio rerio cdna clone 10E17 5', mRNA sequence.
ACCESSION AA495217
VERSION AA495217.1 GI:2225645
KEYWORDS EST.
SOURCE zebrafish.
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Rasbora; Danio.
REFERENCE 1 (bases 1 to 404)
AUTHORS Clark, M., Lehrach, H., Appel, B., Eisen, J., Johnson, S., Marra, M., Eddy, S., Hillier, L., Allen, M., Bowles, L., Dubuque, P., Gelsel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Willson, R.
TITLE WashU zebrafish EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Steve Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha; Holacanthopterygii; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

1 (bases 1 to 1110)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizes, C., Fisher, C., Bouneau, L., Billaud, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.

Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

Unpublished

2 (bases 1 to 1110)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizes, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence

Unpublished

3 (bases 1 to 1110)

Genoscope.

Direct Submission

Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.

FEATURES

Source

1..1110

/organism="Tetraodon nigroviridis"

/db_xref="taxon:99883"

/clone="042M15"

/clone_lib="C"

/note="Genoscope sequence ID : C0BC042AG08T1-end : T3"

BASE COUNT 222 a 293 c 292 g 281 t 22 others

ORIGIN

Query Match 7.5%; Score 95; DB 193; Length 1110;

Best Local Similarity 70.6%; Pred. No. 7.4e-17;

Matches 139; Conservative 0; Mismatches 57; Indels 1; Gaps 1;

QY 179 aggaatgtggttcgctatggggagagtgacagtgctgtgacgtgcccggctgcacaggt 238

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 706 AGGAATGTGGCTTTGGCTCGGAGAGGATGCCGGTGTGTGCTTCGGAGCGCGCT 765

QY 239 tcaagagagactgggcttccagaataaagccctgtctgactgcagtggtgaacc 298

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 766 TCAAGAGGAGCGCGNCTGCAGAGTGCAGGCGCTTCGCTGGACTGCGGCTCATCAACC 825

QY 299 gcttcagaaggaataattgttcagccagctgactgactct-gcgggagctgttgcca 357

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 826 GCTTCAGAGGCGCACTGCTCCACCAGCAGCAACGACGTNTGTTGGAGACTGCTGCC 885

QY 358 ggatttatagggaagac 374

||| |||||

Db 886 GGCTCAGTCAGCAGGCC 902

RESULT 15

AW527025/c

LOCUS

DEFINITION

UI-R-B01-ajg-f-10-0-UI.s1 UI-R-B01 Rattus norvegicus cDNA clone

UI-R-B01-ajg-f-10-0-UI 3', mRNA sequence.

ACCESSION

AW527025

VERSION

AW527025.1

GI:7169439

KEYWORDS

EST.

SOURCE

Norway rat.

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus

1 (bases 1 to 414)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

TITLE

JOURNAL

MEDLINE

COMMENT

Normalization and subtraction: two approaches to facilitate gene discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

Contact: Soares, MB

Program for Rat Gene Discovery and Mapping

University of Iowa

451 Eckstein Medical Research Building Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized mid-brain library cDNA Library Preparation: M.B. Soares

Lab Clone Distribution: clones will be available through Research Genetics (www.resgen.com)

Seq primer: M13 Forward

POLYA=Yes.

FEATURES

Location/Qualifiers

1..414

/organism="Rattus norvegicus"

/strain="Sprague-Dawley"

/db_xref="taxon:10116"

/clone="UI-R-B01-ajg-f-10-0-UI"

/clone_lib="UI-R-B01"

/dev_stage="adult"

/lab_host="DH10B (Life Technologies)"

/note="Vector: pT73D-pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The library (UI-R-B01) is a subtracted library derived from a mixture of the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons, midbrain, cerebral cortex, corpus striatum and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at ratseq.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)

6:791-806, 1996)

TAG_LIB=UI-R-B01

TAG_TISSUE=mid-brain

TAG_SEQ=GATGG"

BASE COUNT 91 a 102 c 94 g 127 t

ORIGIN

Query Match 7.2%; Score 91.2; DB 91; Length 414;

Best Local Similarity 58.5%; Pred. No. 6.9e-16;

Matches 159; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY 975 ttatcctgaactcactggagagacattctctcaatccagaactgaaagctcaac 1034

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 414 TTATCTCTGAACCTCACTGGAGAGATATCAATCCCTCAATCCGAAATGAAGCTCAAC 355

QY 1035 gtcttggattcaaatagcagcaagattgtgtgggtgttccagtcagtcctca 1094

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 354 ATCTGTGGATTCCAAATGGTGTGAGTGTGGTGGGGAGCTGCTCCAGATTCTTCTCG 295

QY 1095 ttctgaaaactttacagcagctactgatttatctatagataaacaacactggtagaatc 1154

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 294 AGATTTTTCAGAAAATATCTGACTCACCTAGATATGCTGAGCCGATACGGTCTGGGAGCA 235

QY 1155 agcatcaactcagatgcactaatgataagagcagctagatcagagagatggtcgctat 1214

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 234 AACCTAGCTCAGGATGCTCAAAGGACTCCAAAGCAGAGAGGCTGGGAAGCCAGTGAATA 175

QY 1215 catccaccagcactcagagctccctccag 1246

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 174 CCTGANTCTAGCCACGCTCCACAGCCTTCCAGG 143

Search completed: March 2, 2001, 09:58:55
Job time: 28920 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 09:58:55 ; Search time 4027.99 Seconds
(without alignments)
2964.446 Million cell updates/sec

Title: US-09-380-276A-2
Perfect score: 1704
Sequence: 1 gggaacgtagaactctccaa.....gaccacagatatacttttc 1704

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues 15983484
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
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 189: em_estpl78:*

190: gb_gss25:*
 191: gb_gss26:*
 192: gb_gss27:*
 193: gb_gss28:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB	ID	Description
1	17.7	302.2	395	106	BE306459	BE306459 601103459
2	16.1	274.8	282	28	AL036000	AL036000 DKFp584K
3	16.1	273.8	454	147	W56629	W56629 xdl6gell.r1
4	15.5	264.8	534	135	BE757704	BE757704 212225 MA
5	12.7	215.6	401	1	AA003356	AA003356 mg4901.r
6	11.3	192.8	369	91	AA078317	AA078317 19558 MAR
7	11.0	186.6	358	1	AA036247	AA036247 ml74803.r
8	9.7	165	325	140	D82546	D82546 HUMHBC4158
9	9.7	165	461	140	D82492	D82492 HUMHBC4526
10	9.7	165	489	140	D82272	D82272 HUMHBC4271
11	9.7	165	515	140	D82308	D82308 HUMHBC4605
12	9.6	164	417	140	D82482	D82482 HUMHBC4476
13	9.4	160	392	140	D82504	D82504 HUMHBC4605 H
14	9.2	157.6	258	133	BB542020	BB542020 BB542020
15	9.1	155	643	159	AQ563354	AQ563354 HS_5335_B
16	8.9	152.4	157	140	D82323	D82323 HUMHBC4706
17	7.4	125.8	646	159	AQ544065	AQ544065 RPCI-11-3
18	7.3	124.4	275	31	AV111112	AV111112 AV111112
19	7.1	120.8	404	8	AA495217	AA495217 fa04d10.r
20	6.7	113.8	450	158	AQ514075	AQ514075 HS_5184_A
21	6.6	112.4	414	91	AW527025	AW527025 UI-R-B01-
22	5.6	95	1110	193	CNS050TC	AL347097 Tetraodon
23	5.1	86.8	381	21	AI551729	AI551729 vflle02.y
24	4.7	80	425	31	AV167843	AV167843 AV167843
25	4.0	67.4	442	109	BE554624	BE554624 ur48c11.y
26	3.5	59	405	150	AQ173919	AQ173919 HS_3204_A
27	3.4	58	485	28	AL120773	AL120773 DKFp762C
28	2.5	42.6	443	11	AA759377	AA759377 ah54a10.s
29	2.4	41.4	551	12	AA814296	AA814296 nz07d08.s
30	2.4	40.2	255	7	AA445805	AA445805 vflle02.r
31	2.3	39.4	397	13	AA860208	AA860208 ak48c10.s
32	2.3	39.4	465	147	W47341	W47341 zc34h02.s1
33	2.3	39.2	266	128	BB350382	BB350382 BB350382
34	2.3	39.2	407	146	W32428	W32428 zc05c12.s1
35	2.3	39	559	3	AA161105	AA161105 zc05c05.s
36	2.3	38.8	706	109	BE535395	BE535395 601058548
37	2.3	38.8	925	190	CNS0091P	AL053013 Drosophila
38	2.3	38.6	502	13	AA925878	AA925878 UI-R-A1-e
39	2.3	38.6	552	134	BE104177	BE104177 UI-R-BX0-
40	2.3	38.6	554	17	AI171746	AI171746 EST217728
41	2.3	38.6	555	17	AI179276	AI179276 EST222969
42	2.2	38.2	1082	193	CNS05NLR	AL345528 Tetraodon
43	2.2	38	391	21	AI522266	AI522266 t184f06.x
44	2.2	38	597	97	AA968349	AA968349 EST380424
45	2.2	37.8	458	88	AA303441	AA303441 xvl9b01.x

ALIGNMENTS

RESULT 1

BE306459

LOCUS

DEFINITION

601103459f1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3495566 5', mRNA sequence.

ACCESION

VERSION

KEYWORDS

SOURCE

BE306459 395 bp mRNA

601103459f1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3495566 5', mRNA sequence.

BE306459

BE306459.1 GI:9159707

EST.

house mouse.

EST

13-JUL-2000

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 454) Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston R., Williamson, A., Wohldmann, P. and Wilson, R.
TITLE	The WashU-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	Contact: Willson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1373 Std Error: 0.00 Seq primer: mob.REGA+ET. Location/Qualifiers 1. .454
FEATURES	
SOURCE	

```

/organism="Homo sapiens"
/db_xref="GDB:1266219"
/db_xref="taxon:9606"
/clone_lib="IMAGE:340844"
/clone_lib="Soares_fetal_heart_NBHH19W"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: heart; Vector: pT7m3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAAGTGGGAGCGCGCATCTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBHL19W."
132 a 88 q 138 t
BASE COUNT 132 a 88 q 138 t

```

Query Match	16.1%	Score 273.8;	DB 147;	Length 454;
Best Local Similarity	99.3%;	Pred. No. 1.6e-70;		
Matches 275;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	1016	ctcttatcctgaaactcactggagaagacattcattctctcaatccagaacttgaagctc	1075
Db	1	CTCTATTCCTGAATCTACTCGAGAAGACATTCAATCTCTCAATCCGAACATTGAAGATC	60
QY	1076	aagctctcttgagatccaatagcagctcaagatttggttggtgggctgttcagtcacgctc	1135
Db	61	AACGCTTTTGATTCGAATAGCAGTCAAGATTTGGTTGGTGGGGCTGTTCAGTCCAGTCT	120
QY	1136	tcattctgaaactttacagcagctactgattctatctagataatacaacacactggtaga	1195
Db	121	TCATTCTGAAAACTTTACAGCAGCTACTGATTTATCTAGATATTAACAACACACTGGGTAGA	180
QY	1196	atcagcatcaactcaggatgcactaactatgagaagccagctagatcaggagagtggcgc	1255
Db	181	ATCAGCATCAACTCAGGATGCACCTAACTATGAGAAGCCAGCTAGATCAGGAGAGTGGGCG	240
QY	1256	tataatccaccagcactcagacgttcctctccagaa	1292
Db	241	TGTCATCCACCCGCCACTCAGACGTCCCTCCAGGTA	277

RESULT 4
BE257704

LOCUS	BE757704	534 bp	mRNA	EST	15-SEP-2000
DEFINITION	212225 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.				
ACCESSION	BE757704				
VERSION	BE757704.1	GI:10171696			
KEYWORDS	EST.				
SOURCE	cow.				
ORGANISM	Bos taurus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
	Bovidae; Bovinae; Bos.				
REFERENCE	1 (bases 1 to 534)				
AUTHORS	Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid ,W.W. and Keele,J.W.				
TITLE	Design and use of four pooled tissue normalized cDNA libraries for EST discovery in cattle				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel.: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov				
	Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.				
	PCR Primers FORWARD: AGGAACAGCTATGACCAT BACKWARD: GTTTCCGAGTCACGACG Plate: 65 row: C column: 2 Seq primer: ATTTAGTGACACTATAG.				
FEATURES	Location/Qualifiers				
source	1. .534 /organism="Bos taurus" /db_xref="taxon:9913" /clone_lib="MARC 2BOV" /tissue_type="pooled" /lab_host="DH10B" /note="Vector: pcMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, thymus, sartendodonus muscle, longissimus muscle, pancreas, adrenal, and endometrium."				
BASE COUNT	122 a 117 c 171 g 124 t				
ORIGIN					

[illegible]

normalization to a Cot = 5. Library constructed by Bento Soares and M.Fátima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."

BASE COUNT 81 a 98 c 110 g

ORIGIN

Query Match 11.0%; Score 186.6; DB 1; Length 358;
Best Local Similarity 77.9%; Pred. No. 1.7e-44;
Matches 225; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 22 aataatcatattgataagaagaggctttaaagtgtactacgaacaagagaaccgt 81
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 69 AATAAACAACGTTTGGTGAGAGCCATGCCTCAAGGTTCCTACCCTACACAGGACGGTGC 128

QY 82 ttttcaccttttagtatcactaggctatttgccatgtaaaagtgacttgtgaacaggag 141
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 129 TCTTCGCTGCCATTCTCCTACTCACCTCGCATGTAAAGTGAGTTCGAACACCGGAG 188

QY 142 actgtagacagcaagaattcaggagtcggctcgaaaactgtctcccgcacacagtggt 201
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 189 ATTGCAGGCAGCAGGAATTCAAAGATCGATCTGGAACTGTGTCCCTCGCAACAGTGGC 248

QY 202 ggccaaggcatggagttgtctaaggaatatggtccttcggctatggggaggatgccacagtg 261
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 249 GACCTGGCATGGAGTTGTCCAAGAATGTGGCTTCGGCTATGGGAGGATGCACAGTGTG 308

QY 262 tgacgtgcggcgtgcacaggttc aaaggaggacgtgggcttccagaanaatg 310
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 309 TGCCCCTGCAGGCCGCACCGGCTTCAAGGAAGACTGGGGTTTTCCAGNAAGTG 357

RESULT 8

D82546 Locus HOMHEC4F58 Human pancreatic islet Homo sapiens EST

DEFINITION D82546

ACCESSION D82546

VERSION D82546.1 GI:1183419

KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Taxonomy ID: 9606 [taxon] | NCBI Taxonomy | UniProt taxonomic classification

REFERENCE
AUTHORS Takeda,J.
TITLE Human pancreatic islet ESTs
JOURNAL Unpublished (1995)
COMMENT Contact: Jun Takeda
Institute for Molecular and Cellular Regulation, Gunma University
3-39-15 Showa-machi, Maebashi Gunma 371, Japan
Tel: 272-20-8856
Fax: 272-20-8896
Email: jtakedaesb.gunma-u.ac.jp.
Location/Qualifiers
1..325
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human pancreatic islet"
I; mRNA was prepared from normal adult human islets. CDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences <100 bp in size."

FEATURES
source

BASE COUNT 97 a 60 c 66 g 99 t 3 others

ORIGIN

Query Match 9.7%; Score 165; DB 140; Length 325;
Best Local Similarity 100.0%; Pred. No. 4.6e-38;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1540 ccatacagaagcttctctgcacaaaaagtcactcaaagcggatgggtgatgcgtgcgc 1599
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1 CCTACATGAGAGCTTCTGCGCACAAAGTGAAGTCTCAAGACGGATGGTTGAGCTGCG 60
QY 1600 agcctatgagattgtggacataatacaagaacagaaatgcctcatctatttttcag 1659
|||||
Db 61 AGCCTATGAGATGTGGACATATACAGAAACAGAAATGCCCTCATGCTTATTTTCATG 120
QY 1660 gtgattgtggttttcaagactgaagaccagagtagtatacttttc 1704
|||||
Db 121 GTGATTGTGGTTTACAGAGTGAAGACCCAGAGTATACTTTTC 165

RESULT 9
LOCUS D82492
DEFINITION HUMHC4526 Human pancreatic islet Homo sapiens cDNA, mRNA sequence.
ACCESSION D82492
VERSION D82492.1 GI:1183664
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 461)

Takeda, J.
Human pancreatic islet ESTs
Unpublished (1995)
Contact: Jun Takeda
Institute for Molecular and Cellular Regulation, Gunma University
3-39-15 Showa-machi, Maebashi Gunma 371, Japan
Tel: 272-20-8856
Fax: 272-20-8896
Email: jtakeda@sb.gunma-u.ac.jp.

FEATURES
source
1. 461
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human pancreatic islet"
/note="Vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences <1000 bp in size."
BASE COUNT 137 a 91 c 96 g 134 t 3 others
ORIGIN

Query Match 9.7%; Score 165; DB 140; Length 461;
Best Local Similarity 100.0%; Pred. No. 5.3e-38;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1540 cctacatgagaagcttctgcccacaaagtgactcaaaagcggatgggtgagctgac 1599
Db 1 CCTACATGAGAGCTTCTGCGCACAAAGTGAAGTCTCAAGACGGATGGTTGAGCTGCG 60
QY 1600 agcctatgagattgtggacataatacaagaacagaaatgcctcatctatttttcag 1659
|||||
Db 61 AGCCTATGAGATGTGGACATATACAGAAACAGAAATGCCCTCATGCTTATTTTCATG 120
QY 1660 gtgattgtggttttcaagactgaagaccagagtagtatacttttc 1704
|||||
Db 121 GTGATTGTGGTTTACAGAGTGAAGACCCAGAGTATACTTTTC 165

RESULT 10
LOCUS D82272
DEFINITION HUMHC4271 Human pancreatic islet Homo sapiens cDNA, mRNA sequence.
ACCESSION D82272
VERSION D82272.1 GI:1183487
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 489)
Takeda, J.
Human pancreatic islet ESTs
Unpublished (1995)
Contact: Jun Takeda
Institute for Molecular and Cellular Regulation, Gunma University
3-39-15 Showa-machi, Maebashi Gunma 371, Japan
Tel: 272-20-8856
Fax: 272-20-8896
Email: jtakeda@sb.gunma-u.ac.jp.

FEATURES
source
1. 489
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human pancreatic islet"
/note="Vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences <1000 bp in size."
BASE COUNT 144 a 94 c 110 g 138 t 3 others
ORIGIN

Query Match 9.7%; Score 165; DB 140; Length 489;
Best Local Similarity 100.0%; Pred. No. 5.4e-38;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1540 cctacatgagaagcttctgcccacaaagtgactcaaaagcggatgggtgagctgac 1599
Db 1 CCTACATGAGAGCTTCTGCGCACAAAGTGAAGTCTCAAGACGGATGGTTGAGCTGCG 60
QY 1600 agcctatgagattgtggacataatacaagaacagaaatgcctcatctatttttcag 1659
|||||
Db 61 AGCCTATGAGATGTGGACATATACAGAAACAGAAATGCCCTCATGCTTATTTTCATG 120
QY 1660 gtgattgtggttttcaagactgaagaccagagtagtatacttttc 1704
|||||
Db 121 GTGATTGTGGTTTACAGAGTGAAGACCCAGAGTATACTTTTC 165

RESULT 11
LOCUS D82308
DEFINITION HUMHC4605 Human pancreatic islet Homo sapiens cDNA, mRNA sequence.
ACCESSION D82308
VERSION D82308.1 GI:1183724
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 515)
Takeda, J.
Human pancreatic islet ESTs
Unpublished (1995)
Contact: Jun Takeda
Institute for Molecular and Cellular Regulation, Gunma University
3-39-15 Showa-machi, Maebashi Gunma 371, Japan
Tel: 272-20-8856
Fax: 272-20-8896
Email: jtakeda@sb.gunma-u.ac.jp.

FEATURES
source
1. 515
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human pancreatic islet"
/note="Vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences <1000 bp in size."

```
BASE COUNT      153 a   102 c   113 g   141 t   6 others
ORIGIN

Query Match      9.7%; Score 165; DB 140; Length 515;
Best Local Similarity 100.0%; Pred. No. 5.5e-38;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1540 cctacatgagaagctctctgcacaaaagtgcattcaagaacgagtggttgagctgac 1599
Db 1 CCTACATGAGAAGCTTCTCTGCCACAAAAGTGACTTCAAAGACGGATGGGTGAGCTGGC 60

QY 1600 agcctatgagattgtgacataaacaagaacagaaatgccctcatgcttatttttc 1659
Db 61 AGCCTATGAGATTGTGCACATATAACAAGAACAGAAATGCCCTCATGCTTATTTTCATG 120

QY 1660 gtgattgtggtttacaagactgaagaccagagtgatactttttc 1704
Db 121 GTGATTGTGGTTTACAAAGACTGAAGACCCAGAGTATACTTTTTC 165

RESULT 12
D82482
LOCUS      417 bp      mRNA      EST      09-FEB-1996
DEFINITION Human pancreatic islet Homo sapiens cDNA, mRNA sequence.
ACCESSION D82482
VERSION   D82482.1 GI:1183621
KEYWORDS EST.
SOURCE    Homo sapiens
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 417)
AUTHORS   Takeda,J.
TITLE     Human pancreatic islet ESTs
JOURNAL   Unpublished (1995)
COMMENT   Contact: Jun Takeda
Institute for Molecular and Cellular Regulation, Gunma University
3-39-15 Showa-machi, Maebashi Gunma 371, Japan
Tel: 272-20-8856
Fax: 272-20-8896
Email: jtakeda@sb.gunma-u.ac.jp.
FEATURES   Location/Qualifiers
            source
            1..392
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="Human pancreatic islet"
            /note="Vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
            I; mRNA was prepared from normal adult human islets. cDNA
            was directionally synthesized from the Xho I in the vector
            to the EcoRI site. cDNA was size fractionated to remove
            sequences <1000 bp in size."
BASE COUNT      126 a   77 c   86 g   122 t   6 others
ORIGIN

Query Match      9.6%; Score 164; DB 140; Length 417;
Best Local Similarity 99.4%; Pred. No. 1e-37;
Matches 164; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1540 cctacatgagaagctctctgcacaaaagtgcattcaagaacgagtggttgagctgac 1599
Db 1 CCTACATGAGAAGCTTCTCTGCCACAAAAGTGACTTCAAAGACGGATGGGTGAGCTGGC 60

QY 1600 agcctatgagattgtgacataaacaagaacagaaatgccctcatgcttatttttc 1659
Db 61 AGCCTATGAGATTGTGCACATATAACAAGAACAGAAATGCCCTCATGCTTATTTTCATG 120

QY 1660 gtgattgtggtttacaagactgaagaccagagtgatactttttc 1704
Db 121 GTGATTGTGGTTTACAAAGACTGAAGACCCAGAGTATACTTTTTC 165

RESULT 13
D82504
LOCUS      392 bp      mRNA      EST      09-FEB-1996
DEFINITION Human pancreatic islet Homo sapiens cDNA, mRNA sequence.
ACCESSION D82504
VERSION   D82504.1 GI:1183160
KEYWORDS EST.
SOURCE    human.
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 392)
AUTHORS   Takeda,J.
TITLE     Human pancreatic islet ESTs
JOURNAL   Unpublished (1995)
COMMENT   Contact: Jun Takeda
Institute for Molecular and Cellular Regulation, Gunma University
3-39-15 Showa-machi, Maebashi Gunma 371, Japan
Tel: 272-20-8856
Fax: 272-20-8896
Email: jtakeda@sb.gunma-u.ac.jp.
FEATURES   Location/Qualifiers
            source
            1..392
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_lib="Human pancreatic islet"
            /note="Vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
            I; mRNA was prepared from normal adult human islets. cDNA
            was directionally synthesized from the Xho I in the vector
            to the EcoRI site. cDNA was size fractionated to remove
            sequences <1000 bp in size."
BASE COUNT      115 a   70 c   84 g   112 t   11 others
ORIGIN

Query Match      9.4%; Score 160; DB 140; Length 392;
Best Local Similarity 97.0%; Pred. No. 1.5e-36;
Matches 160; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1540 cctacatgagaagctctctgcacaaaagtgcattcaagaacgagtggttgagctgac 1599
Db 1 CCTACNTGAGAAGCTTCTCTGCCACNAAAGTGACTTCNAAAGCGGATGGGTGAGCTGGC 60

QY 1600 agcctatgagattgtgacataaacaagaacagaaatgccctcatgcttatttttc 1659
Db 61 AGCCTATGAGATTGTGCACATATAACNAGAACAGAAATGCCCTCATGCTTATTTTCATG 120

QY 1660 gtgattgtggtttacaagactgaagaccagagtgatactttttc 1704
Db 121 GTGATTGTGGTTTACAAAGACTGAAGACCCAGAGTATACTTTTNTC 165

RESULT 14
BB542020
LOCUS      258 bp      mRNA      EST      31-JUL-2000
DEFINITION RIKEN full-length enriched, 0 day neonate eyeball Mus
musculus cDNA clone E130118G08 3', mRNA sequence.
ACCESSION BB542020
VERSION   BB542020.1 GI:9613243
KEYWORDS EST.
SOURCE    house mouse.
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 258)
AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.,
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
Y., Shigemoto,Y., Shingawa,A., Shiraki,T., Sogabe,Y., Suganara,Y.,
```

Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watanabe, S., Yamamoto, T., Yamamoto, T., Yamamoto, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Kono, H., et al.)
Unpublished (2000)

TITLE JOURNAL COMMENT

Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
The Institute of Physical and Chemical Research (RIKEN), Genomic
Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-res@rtc.riken.go.jp,
URL: http://genome.rtc.riken.go.jp/
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermotabilization and thermoactivation of thermostable enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsuai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

FEATURES source

Location/Qualifiers
1. .258
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="E130118G08"
/clone_lib="RIKEN full-length enriched, 0 day neonate
eyeball"
/tissue_type="eyeball"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGCGCGCAACTCGAGTGTGTTTGTGTTT 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGAGAGATTCTCGAGTTAATTAATATCCCTCCCTCCCTCC 3']. cDNA
was cleaved with BamHI and XhoI. Vector: a modified
pBluescript KS(+) after bulk excision from Lambda FLC I."
BASE COUNT 55 a 77 C 66 G 60 T
ORIGIN

Query Match 9.2%; Score 157.6; DB 133; Length 258;
Best Local Similarity 80.7%; Pred. No. 6.8e-36;
Matches 184; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
Qy 265 cgtgcgcgtgcacaggttcgaaggaggtggggttcacagaaatgcagccgtgtgtg 324
Db 1 CCTGCAGCCCCACCGGTTCTAAGAAGACTGGGCTTTCAGAAAGTGAAGCCATGTGGCG 60
Qy 325 actgcgcagtggtgacacgctttcagaaggcaaatgtttcagccaccagtgatgcatct 384
Db 61 ACTTTTGGCGTGTGAACCGCTTTCAGAGGCCCCAACTGTCTACACAACTGATGCTTTT 120
Qy 385 gcggggactgcttgcgcaggttttataggaagacgaactgtcggtttcagacatgg 444

Db 121 CGGGGACTGCTGCAGGATTTTACCGAAGAACCAAACTGTTGTTTCAAGACATGG 180
Qy 445 agtgtgtgctgtgagagacctctctctctctctctctctctctctctctctctctctg 492
Db 181 AGTGTGCTCCCTGGGAGAGACCCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 228

RESULT 15

AQ563354 643 bp DNA GSS 29-MAY-1999
LOCUS HS_5335_B2_B03_T7A RPCI-11 Human Male BAC Library Homo sapiens
DEFINITION genomic clone Plate=911 Col=6 Row=D, DNA sequence.
ACCESSION AQ563354
VERSION AQ563354.1 GI:4922825
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 643)
AUTHORS Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Hood, L.

Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Research Genetics (<http://inforesgen.com>). BAC end Web Server:
<http://www.htsc.washington.edu>
Plate: 911 row: D column: 6
Seq primer: T7
Class: BAC ends
High quality sequence stop: 643.

FEATURES source

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Search completed: March 2, 2001, 09:59:02
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

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Run on: March 2, 2001, 12:59:17 ; Search time 8955.7 Seconds
(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 1118133 seqs, 6853842396 residues
Total number of hits satisfying chosen parameters: 2236266

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1256.2	99.0	1489	37	AF167555	AF167555 Homo sapi
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4	729.2	57.5	1678	11	AF167552	AF167552 Mus muscu
5	680.8	53.6	1075	11	AF173166	AF173166 Mus muscu
6	449	35.4	744	11	AB040433	AB040433 Mus muscu
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8	428.8	33.8	143608	67	AL161422	AL161422 Homo sapi
9	428.8	33.8	178256	66	AL139080	AL139080 Homo sapi
10	314	24.7	591	11	AF167554	AF167554 Mus muscu
11	73	5.8	188351	67	AL353136	AL353136 Homo sapi
12	73	5.8	205736	51	AC023560	AC023560 Homo sapi
13	65.4	5.2	205736	51	AC023560	AC023560 Homo sapi
14	43.6	3.4	160214	54	AC034198	AC034198 Homo sapi
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27 37.6 3.0 186797 49 AC021965
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30 37.4 2.9 73868 55 AC055762
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37 36.6 2.9 166712 39 AC012213
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SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Kojima,T., Morikawa,Y., Copeland,N.G., Gilbert,D.J., Jenkins,N.A.,
Senba,E. and Kitamura,T.
TITLE TROY, a newly identified member of the tumor necrosis factor
receptor superfamily, exhibits a homology with Edar and is
expressed in embryonic skin and hair follicles
J. Biol. Chem. 275 (27), 20742-20747 (2000)
20347167
2 (bases 1 to 1364)
AUTHORS Kojima,T. and Kitamura,T.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-2000) to the DDBJ/EMBL/GenBank databases, Tetsuo
Kojima, Chugai Research Institute for Molecular Medicine, Inc.,
Cytochrome Research Program; 153-2 Nagai, Niihari, Ibaraki 300-4101,
Japan (E-mail:kojima@ci.med.tokai.ac.jp, Tel:81-298-306211,
Fax:81-298-306270)
COMMENT Sequence updated (06-Apr-2000).
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REFERENCE 1 (bases 1 to 1489)
AUTHORS Eby,M.F., Jasmin,A., Kumar,A., Sharma,K. and Chaudhary,P.M.
TITLE TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
Activates the c-Jun N-terminal Kinase Pathway and Mediates
Caspase-Independent Cell Death
J. Biol. Chem. 275 (20), 15336-15342 (2000)
10809768
2 (bases 1 to 1489)
AUTHORS Chaudhary,P.M.
TITLE Direct Submission
JOURNAL Submitted (12-JUL-1999) Internal Medicine, UT Southwestern Medical
Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8593, USA
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SOURCE house mouse.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1678)
AUTHORS Eby, M.T., Jasmin, A., Kumar, A., Sharma, K. and Chaudhary, P.M.
TITLE TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
Activates the c-Jun N-terminal Kinase Pathway and Mediates
Caspase-Independent Cell Death
J. Biol. Chem. 275 (20), 15336-15342 (2000)
PUBMED 10809768
REFERENCE 2 (bases 1 to 1678)
AUTHORS Chaudhary, P.M.
TITLE Direct Submission
JOURNAL Submitted (12-JUL-1999) Internal Medicine, UT Southwestern Medical
Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8593, USA
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TPSGGGWREDNLNLMPTAFQDA"
BASE COUNT 371 a 467 c 466 g 374 t
ORIGIN
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Query Match 57.5%; Score 729.2; DB 11; Length 1678;
Best Local Similarity 74.6%; Pred. No. 2.5e-186;
Matches 930; Conservative 0; Mismatches 313; Indels 3; Gaps 1;

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QY 1 atggccttaaaagtctactagaacaagagaaaagcttttccacttttttagtattacta 60
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Db 72 ATGGCACTCAAGTCTCTACTCTACACAGGACGGTGCTCTTCGTCGCCATTCCTTCCTA 131
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QY 61 ggcctatttgatgtaaaagtactgtgaaacagagagactgtagacagcaagaattcagg 120
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Db 132 CTCCACCTGGCATGTAAGTAGTTCGGAACACCGGAGATTGGCAGCAGCAGCAATTCAAG 191
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QY 121 gatcggctcgaacatgtgttccctcgcaaccagtgctggcgagcgatggagtgtctaag 180
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Db 192 GATCGATCTGGAACATGTGTCTCTGTCAAAACAGTGGCGACCTGGCATGGAGTTGTCCAAG 251
QY 181 gaattggcttcggctatgggagagatcacagatgtgagcgtgcgagctcacaggttc 240
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QY 361 ttatatagaagagaaaacttgcgctttcaagacatggaagtgtgccttgcctgtgagaac 420
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Db 432 TTTTACCAGGAAGACCAAACTGGTTGGTTTTCAAGACATGGAGTGTGCCCTGCCGAGAC 491
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QY 421 cctcctcctcttacgaaccgcactgtgccagcaaggtcaacctcgtgaaagatcgctcc 480
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QY 601 aaaccacgctggtctcctgcgggtcacagacattcagtaacacggcctctgagctgtcggt 660
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Db 672 AAACCCAGCTGGTCTCTGGGTCACAGGACATTCAGTACAATGGCTCTGAGCTGTCTATGC 731
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QY 661 cttagacacactcagctccacgaatatgccacagagcgtcgtccagtcgcgcgtgac 720
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QY 721 tcagtcagacacctcgggcggcgtgcgttgcctcccatcctatgctgtgagagagcctgc 780
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Db 912 AACCCGGCTTCTGTGGGGAACACGATGCCAGCTTCTTTGGGCTCTGTTTCCGTTCCATC 971
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Db 1029 TCTCTCTGTGACTCTTATCTGAACCTCACTGGAGAAGATACCAATTCCTCAATCCGAA 1088
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```

```
RESULT 5
AF173166 1075 bp mRNA ROD 26-DEC-1999
LOCUS Mus musculus TNFRSF19 mRNA, complete cds.
DEFINITION AF173166
ACCESSION AF173166
VERSION AF173166.1 GI:6635354
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1075)
AUTHORS Hu.S., Tamada,K., Ni,J., Vincenz,C. and Chen,L.
TITLE Characterization of TNFRSF19, a novel member of the tumor necrosis
factor receptor superfamily
JOURNAL Genomics 62 (1), 103-107 (1999)
MEDLINE 2054362
REFERENCE 2. (bases 1 to 1075)
AUTHORS Hu.S.
TITLE Direct Submission
JOURNAL Submitted (29-JUL-1999) Department of Immunology, Mayo Clinic and
Foundation, 200 First Street SW, Rochester, MN 55905, USA
FEATURES
source
Location/Qualifiers
1..1075
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TVSSPRDLAAVICSALATVLLALLILCVYKRFMEKPPSWLSRPQDIQYNGSEL
SCFDQPRLRHCAHRACQYHRDAPMYGPVHLIPSLCCEEARSSARAVLGGRLSPPT
LOERNPASVGNTPAFFGVSRSICAEFSDAWPLMQNPLGGDSSLCDSPVELTGEDTN
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BASE COUNT 211 a 308 c 296 g 259 t 1 others
ORIGIN
Query Match 53.6%; Score 680.8; DB 11; Length 1075;
Best Local Similarity 78.9%; Pred. No. 3 le-173;
Matches 824; Conservative 0; Mismatches 217; Indels 3; Gaps 1;
QY 1 atggcgttaaaagtgtactagacaagagaaaacgtttttcactcttttagtattacta 60
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QY 121 gatcgtctggaaaactgtgtcctcgaaccagtggtggccaggcagtgagttgtctaag 180
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Db 148 GATCGATCTGGAACACTGTCTCTCTGCAACAGTGGCGGACCTGGCATGGAGTTGTCCAAG 207
QY 181 gaatgtggttcgtgggtatggggaggatgcacagtggtgtgacgtgctggcaggttc 240
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Db 208 GAATGTGGTTCGGCTATGGGAGGATGCACAGTGTGTGCCCTGCGAGCGCGACCGGTTTC 267
QY 241 aaggaggaactggggcttcagaaaatgcagccctgtctggaactgcagtggtgaaaccgc 300
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Japan (E-mail: kojimat@immed.com, Tel: 81-298-306211,
Fax: 81-298-306270)

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FEATURES
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BASE COUNT    162 a    208 c    211 g    163 t
ORIGIN
Query Match      35.4%; Score 449; DB 11; Length 744;
Best Local Similarity 82.4%; Pred. No. 1.5e-110;
Matches 515; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
QY 1 atggttttaaaagtctactagaagaagaaacggtttttcactcttttagtattacta 60
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QY 61 ggctatttgcataaagtctgtgaacagagagactgtagacagaagaattcaag 120
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Db 127 CTCACCTGGCATGTAAGTGTGCGAACCAGGAGATTGACGACGACGAATTCAG 186
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Db 187 GATCGATCTGGAACTGTCTCTCTGCAACACAGTCGGGACCTGGCATGGAGTTGTC 246
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QY 181 gaatgtggttcggctatggggaggagatgcacagtggtgacgtgcggcgtgcacaggttc 240
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Db 247 GAATGTGGCTTCGGGTATGGGAGGATGCACAGTGTGTGCTGCCCTGCAGCCGACCG 306
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QY 241 aaggagactggggtcttcagaaatgcagaccctgtctgagactgcgcagtggtgaaccgc 300
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QY 301 ttccagaaggaactgtttcagccaccagtgatgccatctgcggggactgcttgccagga 360
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QY 361 tttttagagaagacgaactctgcgcttttaagacatgagtggtgtgcttgtggagac 420
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Db 427 TTTTACGGGAAGACCAAACTGTTGGTTTTCAGACATAGGAGTGTGTGCCCTCGGAGAC 486
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QY 421 cctcctctcctctagaaacgcactgtgcccagcaaggtcaacctcgtgaagatcgctcc 480
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Db 487 CCACCTCTCTCTTACGAACACCACTGTACACAGAGGTGAACCTGTGGAAGATCTCTCC 546
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QY 481 acggcctccagccacgggacacggcgctggtgctgtattctgcagcgcctctggccacc 540
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Db 607 GTGCTCTCGCCCTGCTCATCTGTGTGTATCTACTGCAAGAGCGAGTTCATGGAGAAG 666
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QY 601 aaacccagctggtctctcggttcac 625
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Db 667 AAACCCAGCTGTAAAGTCCCATCC 691
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```

```
RESULT 7
LOCUS AF167553 886 bp mRNA ROD 25-MAY-2000
DEFINITION Mus musculus TAJ-alpha short mRNA, complete cds.
ACCESSION AF167553
VERSION AF167553.1 GI:8071639
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 886)
Eby, M.T., Jasmin, A., Kumar A., Sharma, K. and Chaudhary, P.M.
TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
Activates the c-Jun N-terminal Kinase Pathway and Mediates
Caspase-independent Cell Death
J. Biol. Chem. 275 (20), 15336-15342 (2000)
10809768
2 (bases 1 to 886)
Chaudhary, P.M.
Direct Submission
Submitted (12-JUL-1999) Internal Medicine, UT Southwestern Medical
Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8593, USA
Location/Qualifiers
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  TVSPRDTALAAVICSALATVLLALLILCVYCKRQPMKKPSKLPCLSLCTVK"
BASE COUNT    204 a    245 c    247 g    190 t
ORIGIN
Query Match      35.4%; Score 449; DB 11; Length 886;
Best Local Similarity 82.4%; Pred. No. 1.5e-110;
Matches 515; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
QY 1 atggttttaaaagtctactagaagaagaaacggtttttcactcttttagtattacta 60
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Db 72 ATGGCACTCAAGGTCCTACTCTACACAGGACGGTGCTCTCGCTGCCATTCTTCTTA 131
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QY 61 ggctatttgcataaagtctgtgaacagagagactgtagacagaagaattcaag 120
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Db 132 CTCACCTGGCATGTAAGTGTGCGAACCAGGAGATTGACGACGACGAATTCAG 191
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QY 121 gatcggtctggaactgtgttccctgcaaccagtggtggccaggcatgagttgtctaa 180
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QY 181 gaatgtggttcggctatggggaggagatgcacagtggtgacgtgcggcgtgcacaggttc 240
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Db 432 TTTTACGGGAAGCAAACTGGTTGGTTTTTCAAGACATGAGTGTGTGCCCTCGGAGAC 491
QY 421 cctcctcctcttaccaacgcactgtgccagagtaacctctgaagatcgcgtcc 480
Db 492 CCACCTCTCCTCCCTACGACCACTGTACCAAGGAGTGAACCTTGTGAAGATCTCCTCC 551
QY 481 acgctccacccacgggacacggcgctggtgcggttatctgcagcgtctggccacc 540
Db 552 ACCGTCTCCAGCCTCGGACACGGCGTGGCTGCCTCATCTGCAGTGTCTGGCCACG 611
QY 541 gtctcgtgcctcgtctcctctctgtgtcatctattgtaagagacagtttatggagaag 600
Db 612 GTCTGCTCCCTCCCTGTCTATCTGTGTCTATCTACTGCAAGAGGCGAGTTTCATGGAGAAG 671
QY 601 aagccagctggtctctgcggtcac 625
Db 672 AAACCCAGCTGTAGCTCCCATCCC 696

RESULT 8
AL161422
LOCUS
DEFINITION Homo sapiens chromosome 13 clone RP11-168G12, *** SEQUENCING IN
PROGRESS ***, 3 unordered pieces.
ACCESSION AL161422
VERSION AL161422
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 143608)
Pearce.A.
Direct Submission
Submitted (19-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Sep 22, 2000 this sequence version replaced gi:10190601.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA168G12
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: pBlasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 143007 bases at least Q40
Consensus quality: 143260 bases at least Q30
Consensus quality: 143347 bases at least Q20
Insert size: 143408; sum-of-contigs
Insert size: 145175; 5.9% error; agarose-fp
Quality coverage: 8.55x in Q20 bases; sum-of-contigs Quality
coverage: 8.58x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1
* 2992 3092: contig of 2992 bp in length
* 3093 129375: gap of 100 bp
* 129376 129475: contig of 126283 bp in length
* 129476 143608: gap of 100 bp
* 129476 143608: contig of 14133 bp in length.
* Location/Qualifiers
* 1. .143608
* /organism="Homo sapiens"
```

```
/db_xref="taxon:9606"
/chromosome="13"
/clone="Rp11-168G12"
/clone_lib="RPC1-11.1"
1. .2992
/note="assembly_fragment:01799
fragment_chain:1"
3093. .129375
/note="assembly_fragment:02957
fragment_chain:1
clone_end:77
vector_side:left"
129476. .143608
/note="assembly_fragment:00106"
200 others

BASE COUNT 41121 a 29506 c 30419 g 42362 t
ORIGIN

Query Match 33.8%; Score 428.8; DB 67; Length 143608;
Best Local Similarity 99.5%; Pred. No. 4.9e-105;
Matches 430; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 838 agaaacgcagggccacggggagatggtgcgacttcttcgagtcacctcagcgatcc 897
Db 84813 AGAAACGCAGGCCCGGAGATGTCGCCGACTTCTTCGGATCCCTCAGCGAGTCC 84872

QY 898 atctgtggcaggttttcagatgcctggcctctgtagcagaatcccatgggtggtgacaac 957
Db 84873 ATCTGTGGCGAGTTTCAGATGCCTGGCCTCTGATCAGAATCCCATGGGTGGTGACAAC 84932

QY 958 atctcttttggactcttctcctgaactcactgagcagtgagagacattctctcctcaatcca 1017
Db 84933 ATCTCTTTTGTGACTCTTATCTCTGAACCTCAGTGGAGAGACATTCTCTCAATCCA 84992

QY 1018 gaactgaaagcctcaacgtcttttggatttcaaaatagcagtcgaagatttgggtggtgggct 1077
Db 84993 GAACTTTGAAAGCTCAACGCTTTTGGATTCAAATAGCAGTCAAGATTGGTTGGTGGGGCT 85052

QY 1078 gtccagtcagctctctctctgaaaactttacagcagcactgactgattcttagatataac 1137
Db 85053 GTTCCAGTCCAGTCTCATCTGAAAACCTTTACAGCAGCTACTGATTATCTAGATATAAC 85112

QY 1138 aaacacactgtagaatcagcatcaactcaggatgcactaactatgagaagccagctagat 1197
Db 85113 AACACACTGTTAGTAATCAGCATCACTCAGGATGCATAACTATGAGAAGCCAGCTAGAT 85172

QY 1198 caggagagtgcgctatcatccaccagccactcagagtcctccctcagtaagagcgagcga 1257
Db 85173 CAGGAGAGTGGTGTCTGTCATCCACCAGCCACTCAGACGCTCCCTCCAGGTAAGCGACGA 85232

QY 1258 ctgggttcctctg 1269
Db 85233 CTGGGTTCCCTG 85244

RESULT 9
AL139080
LOCUS
DEFINITION Homo sapiens chromosome 13 clone RP11-173N17 map q12.11-12.3, ***
SEQUENCING IN PROGRESS ***, 15 unordered pieces.
ACCESSION AL139080
VERSION AL139080.8 GI:10443032
KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 178256)
Burton.J.
Direct Submission
Submitted (28-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
```

COMMENT

On Oct 1, 2000 this sequence version replaced gi:10129398.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: ba173N17
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 168976 bases at least Q40
Consensus quality: 172107 bases at least Q30
Consensus quality: 173780 bases at least Q20
Insert size: 176856; sum-of-contigs
Insert size: 163577; 8.6% error; agarose-fp
Quality coverage: 3.73x in Q20 bases; sum-of-contigs Quality
coverage: 4.07x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1
* 8224 8223: gap of 100 bp
* 8324 25426: contig of 17103 bp in length
* 25427 25526: gap of 100 bp
* 25527 28263: contig of 2737 bp in length
* 28264 28363: gap of 100 bp
* 28364 34273: contig of 5910 bp in length
* 34274 34373: gap of 100 bp
* 34374 42235: contig of 7862 bp in length
* 42236 42335: gap of 100 bp
* 42336 53917: contig of 11582 bp in length
* 53918 54017: gap of 100 bp
* 54018 71972: contig of 17955 bp in length
* 71973 72072: gap of 100 bp
* 72073 81711: contig of 9639 bp in length
* 81712 81811: gap of 100 bp
* 81812 88644: contig of 6833 bp in length
* 88645 88744: gap of 100 bp
* 88745 95048: contig of 6304 bp in length
* 95049 95148: gap of 100 bp
* 95149 107455: contig of 12307 bp in length
* 107456 107555: gap of 100 bp
* 107556 125465: contig of 17910 bp in length
* 125466 125565: gap of 100 bp
* 125566 140008: contig of 14443 bp in length
* 140009 140108: gap of 100 bp
* 140109 144761: contig of 4653 bp in length
* 144762 144861: gap of 100 bp
* 144862 178256: contig of 33395 bp in length.
Location/Qualifiers
1..178256

FEATURES

source

/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="13"
/map="q12.11-12.3"
/clone="RP11-173N17"
/clone_lib="RPC1-11.1"
1..8223
/note="assembly_fragment:01724
fragment_chain:1"
8324..25426
/note="assembly_fragment:00074
fragment_chain:1"
25527..28263
/note="assembly_fragment:01884
fragment_chain:1"

misc_feature

misc_feature

misc_feature

misc_feature
28364..34273
/note="assembly_fragment:00979
fragment_chain:1"
misc_feature
34374..42235
/note="assembly_fragment:00126
fragment_chain:2"
misc_feature
42336..53917
/note="assembly_fragment:00364
fragment_chain:2"
misc_feature
54018..71972
/note="assembly_fragment:01769
fragment_chain:2"
misc_feature
72073..81711
/note="assembly_fragment:00399
fragment_chain:3"
misc_feature
81812..88644
/note="assembly_fragment:01132
fragment_chain:3"
misc_feature
88745..95048
/note="assembly_fragment:01416
fragment_chain:3"
misc_feature
95149..107455
/note="assembly_fragment:00061
fragment_chain:4"
misc_feature
107556..125465
/note="assembly_fragment:00302
fragment_chain:4"
misc_feature
125566..140008
/note="assembly_fragment:01438
fragment_chain:5"
misc_feature
140109..144761
/note="assembly_fragment:01533
fragment_chain:5"
misc_feature
144862..178256
/note="assembly_fragment:01008"
BASE COUNT 52999 a 37393 c 36460 g 49998 t 1406 others
ORIGIN

Query Match 33.8%; Score 428.8; DB 66; Length 178256;
Best Local Similarity 99.5%; Pred. No. 4.9e-105;
Matches 430; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 838 aqaacgcagccgcccgggagatggtgcgactttcttcgagtcctccacgactcc 897
|||||
Db 46631 AGAAACGCAGGCCCGGAGATGGTGGCGGACTTTCTCGGATCCCTCAGCAGTCC 46690
|||||

QY 898 atctgtgcgagttttcagatgcctggcctctgatgcagaatcccatgggtgtagaac 957
|||||
Db 46691 ATCTGFGCGAGTTTTCAGATGCTGGCTCTGATGCAGATCCCATGGTGGTGCACAC 46750
|||||

QY 958 atctcttttctgactcttctgaactcactgcagagacattcattctctcaatcca 1017
|||||
Db 46751 ATCTCTTTTGTGACTCTTATCTCTGAACCTCACTGGGAGAGACATTCAATCTCTCAATCCA 46810
|||||

QY 1018 gaacttgaagactcaactcttttgattcaataagacagtcagattggttggtggtc 1077
|||||
Db 46811 GAACITGAAAGCTCAACGTCITTTGGATTCAAATAGCAGTCAAGATTTGGTGGGGCT 46870
|||||

QY 1078 gtccagctcagctctcattctgaaactttacagcagctactgatttattctagataaac 1137
|||||
Db 46871 GTTCCAGTCCAGCTCATCTCTGAAACTTTTACAGCAGCTACTGATTTATCTAGATATAAC 46930
|||||

QY 1138 aacacactggttagaatacagcactcaactcaggtatgcactaatatgagagccagctagat 1197
|||||
Db 46931 AACACACTGGTAGAAATCAGCATCACTCAGATGCTCACTAATCACTATGAGAAAGCCAGCTAGAT 46990
|||||

QY 1198 caggagagtgccgttatccaccagcactcagcagcctccctccctcagtagagcagca 1257
|||||
Db 46991 CAGGAGAGTGGTGTGTGTCTCACCAGCCAGCTCAGACGCTCCCTCCAGGTAAAGGCAGCGA 47050
|||||

QY 1258 ctgggttccctg 1269

FEATURES	SOURCE
1. High Accuracy: The model achieves a high accuracy rate, indicating its effectiveness in predicting the target variable.	Model Performance Metrics
2. Robustness: The model demonstrates robustness against various input variations and noise, ensuring reliable predictions.	Model Performance Metrics
3. Interpretability: The model's predictions are interpretable, allowing users to understand the underlying factors influencing the outcome.	Model Performance Metrics
4. Scalability: The model is scalable, capable of handling large volumes of data and complex tasks efficiently.	Model Performance Metrics
5. Real-time Processing: The model supports real-time data processing, enabling immediate insights and decision-making.	Model Performance Metrics
6. Integration with Existing Systems: The model seamlessly integrates with existing data systems and workflows, facilitating easy adoption.	Model Performance Metrics
7. Customizable Parameters: The model offers customizable parameters, allowing users to tailor the model to specific requirements.	Model Performance Metrics
8. Comprehensive Documentation: The model is accompanied by comprehensive documentation, providing detailed information on its usage and capabilities.	Model Performance Metrics
9. Regular Updates: The model is regularly updated with the latest data and algorithms, ensuring its performance remains state-of-the-art.	Model Performance Metrics
10. Support and Training: The model is supported by a dedicated team, offering training and assistance to users.	Model Performance Metrics

```
1. 203750
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
/map="17"
```

[illegible]


```

1. /db_xref="taxon:9606"
/organism="Homo sapiens"
/chromosome="17"
/map="17"
/clone="RP11-85120"
/clone_lib="PC1-11 Human Male BAC"
1. .1267
/note="assembly_fragment"
1368. .2402
/note="assembly_fragment"
2503. .3524
/note="assembly_fragment"
3625. .4913
/note="assembly_fragment"
5014. .6289
/note="assembly_fragment"
6390. .7655
/note="assembly_fragment"
7756. .9267
/note="assembly_fragment"
9368. .11138
/note="assembly_fragment"
11239. .13822
/note="assembly_fragment"
13923. .16968
/note="assembly_fragment"
17069. .20185
/note="assembly_fragment"
20286. .22634
/note="assembly_fragment"
22735. .27012
/note="assembly_fragment"
27113. .29342
/note="assembly_fragment
clone_end:T7
vector_side:right"
29443. .33381
/note="assembly_fragment"
33482. .36562
/note="assembly_fragment"
36663. .40982
/note="assembly_fragment"
41083. .45520
/note="assembly_fragment"
45621. .50623
/note="assembly_fragment"
50724. .55610
/note="assembly_fragment"
55711. .61038
/note="assembly_fragment"
61139. .66159
/note="assembly_fragment"

```

```

* 138441 138540: gap of unknown length
* 138541 160214: contig of 21674 bp in length.
FEATURES
    source
        1..160214
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="3"
            /map="3p"
            /clone="RP11-767C1"
            1..1071
                /note="assembly_name:Contig7"
            1172..2254
                /note="assembly_name:Contig10"
            2355..3851
                /note="assembly_name:Contig12"
            3952..5295
                /note="assembly_name:Contig13"
            5396..6465
                /note="assembly_name:Contig14"
            6566..7857
                /note="assembly_name:Contig15"
            7958..9194
                /note="assembly_name:Contig16"
            9295..11038
                /note="assembly_name:Contig17"
            11139..14420
                /note="assembly_name:Contig18"
            14321..17864
                /note="assembly_name:Contig19"
            17965..21270
                /note="assembly_name:Contig20"
            21371..25050
                /note="assembly_name:Contig21"
            clone_end:T7
            vector_side:right"
            25151..30624
                /note="assembly_name:Contig23"
            30725..37771
                /note="assembly_name:Contig24"
            clone_end:SP6
            vector_side:left"
            37872..42147
                /note="assembly_name:Contig25"
            42248..49752
                /note="assembly_name:Contig26"
            49853..57293
                /note="assembly_name:Contig27"
            57394..63626
                /note="assembly_name:Contig28"
            63727..72520
                /note="assembly_name:Contig29"
            72621..83538
                /note="assembly_name:Contig30"
            83639..95213
                /note="assembly_name:Contig31"
            95314..107621
                /note="assembly_name:Contig32"
            107722..120511
                /note="assembly_name:Contig33"
            120612..138440
                /note="assembly_name:Contig34"
            138541..160214
                /note="assembly_name:Contig35"
BASE COUNT 40339 a 38297 c 38619 g 40533 t 2426 others
ORIGIN

Query Match          3.4%;   Score 43.6;  DB 54;   Length
Best Local Similarity 48.4%;   Pred. No. 0.74;  129;   Indels
Matches 121;  Conservative  0;   Mismatches

Qy  637 tacaacgctctgagctgtctgtcttgtagacagacctcagctccacgaataatg
      |||||

```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 12:42:21 ; Search time 553.05 Seconds
(without alignments)
861.976 Million cell updates/sec

Title: US-09-380-276A-5

Perfect score: 1269

Sequence: 1 atggttttaaaagtgtact.....ggcagcgactgggttcctg 1269

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 18781343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_36:*

- 1: /SID56/gcgdata/geneseq/geneseq/NA1980.DAT:*
- 2: /SID56/gcgdata/geneseq/geneseq/NA1981.DAT:*
- 3: /SID56/gcgdata/geneseq/geneseq/NA1982.DAT:*
- 4: /SID56/gcgdata/geneseq/geneseq/NA1983.DAT:*
- 5: /SID56/gcgdata/geneseq/geneseq/NA1984.DAT:*
- 6: /SID56/gcgdata/geneseq/geneseq/NA1985.DAT:*
- 7: /SID56/gcgdata/geneseq/geneseq/NA1986.DAT:*
- 8: /SID56/gcgdata/geneseq/geneseq/NA1987.DAT:*
- 9: /SID56/gcgdata/geneseq/geneseq/NA1988.DAT:*
- 10: /SID56/gcgdata/geneseq/geneseq/NA1989.DAT:*
- 11: /SID56/gcgdata/geneseq/geneseq/NA1990.DAT:*
- 12: /SID56/gcgdata/geneseq/geneseq/NA1991.DAT:*
- 13: /SID56/gcgdata/geneseq/geneseq/NA1992.DAT:*
- 14: /SID56/gcgdata/geneseq/geneseq/NA1993.DAT:*
- 15: /SID56/gcgdata/geneseq/geneseq/NA1994.DAT:*
- 16: /SID56/gcgdata/geneseq/geneseq/NA1995.DAT:*
- 17: /SID56/gcgdata/geneseq/geneseq/NA1996.DAT:*
- 18: /SID56/gcgdata/geneseq/geneseq/NA1997.DAT:*
- 19: /SID56/gcgdata/geneseq/geneseq/NA1998.DAT:*
- 20: /SID56/gcgdata/geneseq/geneseq/NA1999.DAT:*
- 21: /SID56/gcgdata/geneseq/geneseq/NA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1269	100.0	1496	19	V33362
2	1267.4	99.9	1502	20	X08689
3	1256.2	99.0	1489	20	X23415
4	1244.8	98.1	1704	19	V33361
5	1240	97.7	2185	20	X24978
6	835.6	65.8	987	20	X59346
7	729.2	57.5	1678	20	X23413
8	449	35.4	886	20	X23414
9	449	35.4	942	20	X24977
10	449	35.4	981	20	X87394
11	435.4	34.3	893	20	X84622
12	362.6	28.6	538	20	X59345

13	361.6	28.5	371	19	V11422	Human secreted pro
14	314	24.7	591	20	X23417	Mouse MAP04-gamma
15	314	24.7	599	20	X24976	Mouse TRAIN-R (sho
16	314	24.7	623	20	X84623	Mouse TNFR superfa
17	314	24.7	636	21	X92408	CDNA encoding murf
18	314	24.7	655	20	X87395	Mouse STRIFE2 (Tan
19	154.8	12.2	932	21	X24111	CDNA encoding huma
20	121.8	9.6	1133	20	X23416	Rat rAPO4-alpha DN
21	90.4	7.1	791	20	X24979	Clone GJ156 encodi
22	87.4	6.9	181	19	V11423	Human secreted pro
23	87.4	6.9	201	20	V86655	EST clone AX92. H
24	82	6.5	396	20	X23418	Mouse MAP04-beta D
25	81.2	6.4	546	21	X2410	CDNA encoding huma
26	77.8	6.1	474	21	X92409	CDNA encoding huma
c	77.4	6.1	474	21	X92409	Gene encoding a su
27	44	3.5	10732	21	A10594	Human TANGO 129 (T
28	37.4	2.9	1290	20	X23121	Human TANGO 129 (T
29	37.4	2.9	2570	20	X23120	Human tumour necro
30	37.4	2.9	2703	21	D00061	Human adrenergic r
31	36.4	2.9	1602	15	Q72217	Truncated human al
32	36.4	2.9	1978	15	Q72212	Human truncated al
33	36.4	2.9	1987	16	T11624	Human alpha-1C adr
34	36.4	2.9	1997	16	T11600	Human alpha-1C adr
35	36.4	2.9	1998	15	Q72213	Human alpha-1C adr
36	36.4	2.9	2004	16	T11599	Human alpha-1C adr
37	36.4	2.9	2005	15	Q72211	Human alpha-1C adr
38	36.2	2.9	330	21	A15982	Human protein clon
39	36.2	2.9	659	21	A15992	Human neurotransmi
40	36.2	2.9	2485	17	T09866	DNA methyltransfer
c	36	2.8	2067	20	V99092	DNA methyltransfer
42	36	2.8	19440	20	V99129	Streptomyces hygro
43	35.6	2.8	1150	20	Z06928	Human cytoskeletal
44	35.2	2.8	1050	21	Z58975	Fragment 41-3 of t
45	35	2.8	326	11	Q05546	

ALIGNMENTS

RESULT 1

V33362

ID V33362 standard; cDNA to mRNA; 1496 BP.

XX

AC V33362;

XX

DT 02-DEC-1998 (first entry)

XX

DE Nucleotide sequence of human beta-OAF065.

XX

Human; beta-OAF065; stroma cell; antibody; inflammatory;
cytokine-mediated disease; rheumatism; ulcerative colitis; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 45..1316

FT

FT /*tag= a

FT /*product= "human beta-OAF065 protein"

FT sig_peptide 45..119

FT /*tag= b

FT mat_peptide 120..1313

FT /*tag= c

FT

FT /*transl_except= (pos:711..713, aa= Pro)

FT /*transl_except= (pos:714..716, aa= Arg)

XX

W09838304-A1.

XX

03-SEP-1998.

XX

26-FEB-1998; 98WO-JP00799.

XX

27-FEB-1997; 97JP-0043143.

XX

PA (ONOY) ONO PHARM CO LTD.

XX Fukushima D, Konishi M, Tada H;
 PI WPI: 1998-481205/41.
 DR P-PSDB; W70387.
 XX
 PT Membrane polypeptide expressed by human stroma cells, and antibodies
 PT recognising it - for treatment of inflammatory and other
 PT cytokine-mediated diseases.
 XX
 PS Disclosure; Pages 40-41; 54pp; Japanese.
 XX
 CC This is the nucleotide sequence of the human beta-OAF065, used in
 CC the method of the invention. The process involves the use of peptides
 CC expressed by stroma cells, and its antibodies are used for in the
 CC prevention and treatment of inflammatory and other cytokine-mediated
 CC diseases such as rheumatism, ulcerative colitis.
 XX
 SQ Sequence 1496 BP; 388 A; 360 C; 372 G; 376 T; 0 other;

Query Match 100.0%; Score 1269; DB 19; Length 1496;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1269; Conservative 0; Mismatches 0; Gaps 0;

QY 1 atggcttttaaaagtgctactagacaagagaaaacgtttttcactcttttagtattacta 60
 DB 45 atggcttttaaaagtgctactagacaagagaaaacgtttttcactcttttagtattacta 104
 QY 61 ggctattttgcataagtgacttgtaaacaggagactgtagacagcaaatcagg 120
 DB 105 ggctattttgcataagtgacttgtaaacaggagactgtagacagcaaatcagg 164
 QY 121 gatcggctcgaacgtgttccctcgaacaggatgtggccaggcatgagttgtctaag 180
 DB 165 gatcggctcgaacgtgttccctcgaacaggatgtggccaggcatgagttgtctaag 224
 QY 181 gaatgtggcttcggctcgtatgggagggatgcacagtgtgtgacgtgcggctgcacagggttc 240
 DB 225 gaatgtggcttcggctcgtatgggagggatgcacagtgtgtgacgtgcggctgcacagggttc 284
 QY 241 aaggaggactggggctccagaatacgaagccctgtctggaactgcgcagtggtgaaccgc 300
 DB 285 aaggaggactggggctccagaatacgaagccctgtctggaactgcgcagtggtgaaccgc 344
 QY 301 ttccagaaggcaaatgttcagccaccagtgatgccatctgcccagactgcttgcaggga 360
 DB 345 ttccagaaggcaaatgttcagccaccagtgatgccatctgcccagactgcttgcaggga 404
 QY 361 ttatatagaagacgaactgtcggctttcaagacatgagtggtgcttctgtgagac 420
 DB 405 ttatatagaagacgaactgtcggctttcaagacatgagtggtgcttctgtgagac 464
 QY 421 cctctcctctcttacgaacgcactgtgccagaaggtcaaacctcgtgaagatcgcgtcc 480
 DB 465 cctctcctctcttacgaacgcactgtgccagaaggtcaaacctcgtgaagatcgcgtcc 524
 QY 481 acgggctccagcccgagacacggcgctggtgcggttatctgcagcgtctggccacc 540
 DB 525 acgggctccagcccgagacacggcgctggtgcggttatctgcagcgtctggccacc 584
 QY 541 gtccgtggtgcccctgtctcctctgtgtcattctattgtaagagacagtttatggagaag 600
 DB 585 gtccgtggtgcccctgtctcctctgtgtcattctattgtaagagacagtttatggagaag 644
 QY 601 aaaccagctgtgtctgtgggttcacaggacattcagataaacggctctgtgagctgtcgtgt 660
 DB 645 aaaccagctgtgtctgtgggttcacaggacattcagataaacggctctgtgagctgtcgtgt 704
 QY 661 cttagacagacctcagctcccaaatatgccacagagcctgtgcagtgccgcagctgac 720
 DB 705 cttagacagacctcagctcccaaatatgccacagagcctgtgcagtgccgcagctgac 764

QY 721 tcagtgacagacctgcggcgccgtgctgtgctcccatccatgtgctgtgagagggcctgc 780
 DB 765 tcagtgacagacctgcggcgccgtgctgtgctcccatccatgtgctgtgagagggcctgc 824
 QY 781 agccccaaaccccggaactcttgggtgtggtgggtgcattcttcgagccagcttctcaggcaaga 840
 DB 825 agccccaaaccccggaactcttgggtgtggtgggtgcattcttcgagccagcttctcaggcaaga 884
 QY 841 aacgacggcccgacggcgaggatggtgcgacactttcttcggatccctcagcagctccatc 900
 DB 885 aacgacggcccgacggcgaggatggtgcgacactttcttcggatccctcagcagctccatc 944
 QY 901 tgtggcgagtttttcagatgcctggcctctgtatgcagaatcccatgggtgtgtgacaacatc 960
 DB 945 tgtggcgagtttttcagatgcctggcctctgtatgcagaatcccatgggtgtgtgacaacatc 1004
 QY 961 tctttttgtgactcttctatcctgaactcactggagagacattcattctctcattccatccagaa 1020
 DB 1005 tctttttgtgactcttctatcctgaactcactggagagacattcattctctcattccatccagaa 1064
 QY 1021 cttgaaagctcaacgtcttttgattcaaatagcagtcgaagatttgggtgtgggctgtt 1080
 DB 1065 cttgaaagctcaacgtcttttgattcaaatagcagtcgaagatttgggtgtgggctgtt 1124
 QY 1081 ccagtcagctctcattctgaaactttacagcagctcactgatttattctagatataaacac 1140
 DB 1125 ccagtcagctctcattctgaaactttacagcagctcactgatttattctagatataaacac 1184
 QY 1141 acactggtagaatcagcatcaactcaggatgcactaactatgagaagccagctagatcag 1200
 DB 1185 acactggtagaatcagcatcaactcaggatgcactaactatgagaagccagctagatcag 1244
 QY 1201 gagagtgccgtatcattccaccagccactcagacgtccctcaggttaaggcagcagctg 1260
 DB 1245 gagagtgccgtatcattccaccagccactcagacgtccctcaggttaaggcagcagctg 1304
 QY 1261 ggttccctg 1269
 DB 1305 ggttccctg 1313

RESULT 2
 X08689
 ID X08689 standard; cDNA: 1502 BP.
 XX
 AC X08689;
 XX
 DT 27-SEP-1999 (first entry)
 XX
 DE Novel nucleotide sequence encoding new protein (Clone AX92_3).
 KW Polynucleotide; protein; nutrition; cytokine; cell proliferation;
 KW cell differentiation; immunostimulation; immunosuppression;
 KW haematopoiesis regulation; tissue growth; activin; inhibin;
 KW chemotaxis; chemokinesis; haemostasis; thrombolysis; receptor;
 KW ligand; anti-inflammatory; tumour suppression; gene therapy; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 51..1322
 FT /*tag= a
 FT /product= "Novel protein"
 XX
 PN WO9920644-A1.
 XX
 PD 29-APR-1999.
 XX
 PF 16-OCT-1998; 98WO-US22034.
 XX
 PR 18-OCT-1997; 97US-0955557.
 XX
 PA (GEMY) GENETICS INST INC.

XX Agostino MJ, Bowman MR, Evans C, Jacobs K, Lavallie ER;
PI McCoy JW, Merberg D, Racie LA, Spaulding V, Treacy M;
XX
DR WPI: 1999-288272/24.
DR P-PSDB; W85724.
XX
PT New polynucleotides encoding secreted human proteins
XX
PS Claim 32; Page 116; 136pp; English.
XX
CC The new human secreted proteins are encoded by polynucleotides
CC obtained from human placenta, adult testes, fetal kidney, fetal
CC brain, adult brain and adult blood cDNA libraries.
CC The polynucleotides and proteins are predicted to have biological
CC activities which would make them suitable for treating, preventing or
CC ameliorating medical conditions in humans and animals. Suggested
CC activities include nutritional activity, cytokine and cell
CC proliferation/differentiation activity, immune stimulating (e.g. as
CC vaccines) or suppressing activity, haematopoiesis regulating
CC activity, tissue growth activity, activin/inhibin activity,
CC chemotactic/chemokinetic activity, haemostatic and thrombolytic
CC activity, receptor/ligand activity, anti-inflammatory activity,
CC cadherin/tumour invasion suppressor activity, and tumour inhibition
CC activity. The polynucleotides are also stated to be useful for gene
CC therapy. The sequences are identified by a secretory leader
CC sequence motif in the polynucleotide and it is thought that the
CC encoded proteins have biological activity by virtue of their secreted
CC nature. This clone was designated AX92_3. A probe for this clone is
CC described in X08704.
XX
SQ Sequence 1502 BP; 388 A; 362 C; 375 G; 377 T; 0 other;

Query Match 99.9%; Score 1267.4; DB 20; Length 1502;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1268; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 atggtttaaagtgctactagaacagagaaacggttttcaactcttttagtattacta 60
Db 51 atggtttaaagtgctactagaacagagaaacggttttcaactcttttagtattacta 110
Qy 61 gctatttgctatgaagtgactgtgaacagagagactgtagacagcaagaattcagg 120
Db 111 ggtatttgctatgaagtgactgtgaacagagagactgtagacagcaagaattcagg 170
Qy 121 gatcggtctggaactgtgtccctgcacacagtggtggccaggtgaggtgtctaaag 180
Db 171 gatcggtctggaactgtgtccctgcacacagtggtggccaggtgaggtgtctaaag 230
Qy 181 gaatggtctcggtatgggagagatgcacagtggtgacgtgcggtgcacaggttc 240
Db 231 gaatggtctcggtatgggagagatgcacagtggtgacgtgcggtgcacaggttc 290
Qy 241 aaggaggactgggtcttcagaaaaatgcagccctgtctggaactgcgagtggtgaaccgc 300
Db 291 aaggaggactgggtcttcagaaaaatgcagccctgtctggaactgcgagtggtgaaccgc 350
Qy 301 ttccagaagcaaatgtgttcagccacagtgatgcacatcggtgggactgcttcaggga 360
Db 351 ttccagaagcaaatgtgttcagccacagtgatgcacatcggtgggactgcttcaggga 410
Qy 361 tttatagaagacaaaactgtcggtcttcaagacatggagtggtgcttggagac 420
Db 411 tttatagaagacaaaactgtcggtcttcaagacatggagtggtgcttggagac 470
Qy 421 cctctctctctttagaaccgacgtgtgccagcaagggtcaaacctggtgaagatcgctcc 480
Db 471 cctctctctctttagaaccgacgtgtgccagcaagggtcaaacctggtgaagatcgctcc 530
Qy 481 acggctctcagccacgggacacgctggtgctgcgttatctgcagcgtctgcccacc 540
Db 531 acggctctcagccacgggacacgctggtgctgcgttatctgcagcgtctgcccacc 590

Qy 541 gtctgtggccctgtctcatctctgtgtcatctattgttaagagacagtttatgagaag 600
Db 591 gtctgtggccctgtctcatctctgtgtcatctattgttaagagacagtttatgagaag 650
Qy 601 aaaccagctgtgtctgtcgggtcagacagacattcagtaacacggctctgagctgtgtg 660
Db 651 aaaccagctgtgtctgtcgggtcagacagacattcagtaacacggctctgagctgtgtg 710
Qy 661 cttagacacacctcagctccaggaatatgccacagagcctgtgccagtcgcgcgtgac 720
Db 711 cttagacacacctcagctccaggaatatgccacagagcctgtgccagtcgcgcgtgac 770
Qy 721 tcaatgcagacctcggcggtgtgctgtgtcccatccatgtgtgtgagagagcctgtg 780
Db 771 tcaatgcagacctcggcggtgtgctgtgtcccatccatgtgtgtgagagagcctgtg 830
Qy 781 agcccaaccggcgactctgt 840
Db 831 agcccaaccggcgactctgt 890
Qy 841 aacgcagaccggcggt 900
Db 891 aacgcagaccggcggt 950
Qy 901 tttgt 960
Db 951 tttgt 1010
Qy 961 tttttgt 1020
Db 1011 tttttgt 1070
Qy 1021 ctgaaagctcaacgtctgt 1080
Db 1071 ctgaaagctcaacgtctgt 1130
Qy 1081 ccagtcctcagctctcattctgt 1140
Db 1131 ccagtcctcagctctcattctgt 1190
Qy 1141 acactgt 1200
Db 1191 acactgt 1250
Qy 1201 gtaggt 1260
Db 1251 gtaggt 1310
Qy 1261 ggttccctg 1269
Db 1311 ggttccctg 1319

RESULT 3
X23415
ID X23415 standard; DNA; 1489 BP.
XX
AC X23415;
XX
DT 18-JUN-1999 (first entry)
XX
DE Human hAPO4-alpha DNA.
XX
KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW developmental abnormality; gestational abnormality; prostate cancer;
KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW apoptosis; human; APO4-alpha; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers

```

CDS      65..1336
FT       /*tag= a
FT       /product= "APO4-alpha"
XX
PN WO9911791-A2.
XX
XX 11-MAR-1999.
XX
PD
XX
XX 04-SEP-1998;   98WO-US18393.
XX PF
XX PR
XX 05-SEP-1997;   97US-0924634.
XX
XX (UNIW ) UNIV WASHINGTON.
XX PA
XX Chaudhary PM;
XX PI
XX WIPI: 1999-205191/17.
XX DR P-PSDB; W93581.
XX
XX New Tumor Necrosis Factor family receptor polypeptides and ligands -
XX useful for diagnosis and treatment of prostate cancer and
XX developmental or gestational abnormalities
XX
XX Example IV; Fig 7C; 156pp; English.
XX
CC This invention describes isolated Tumor Necrosis Factor (TNF) family
CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC their active fragments. APO4 is useful for diagnosing prostate cancer
CC by determining levels of APO4 in an individual. Prostate cancer can also
CC be treated using APO4 selective binding agents linked to a therapeutic
CC moiety. APO4 polypeptides are also useful for identifying selective
CC binding agents, useful in diagnosis/treatment of disease by binding of
CC agents to the polypeptide/active fragment which is extracellular, or
CC expressed on the cell surface. The binding is preferably performed in
CC vivo. APO4 polypeptides/ active fragments are also useful for screening
CC for agonists and antagonists by binding and observing the change in APO4
CC activity. Effective pharmacological agents useful in diagnosis or
CC treatment of disease are also identified using APO4 polypeptides/active
CC fragments and APO4 signal transducer molecules that specifically interact
CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC activity. The method is performed in vivo or in vitro. APO polypeptides
CC are all useful as immunogens for preparing antibodies. APO4 is also
CC useful for diagnosis/treatment of developmental or gestational
CC abnormalities. APO8 was transfected to human breast carcinoma cell line
CC MCF-7, and induced apoptosis.
XX
XX Sequence 1489 BP; 361 A; 366 C; 380 G; 382 T; 0 other;
XX SQ

Query Match          99.0%; Score 1256.2; DB 20; Length 1489;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1261; Conservative 0; Mismatches 8; Indels 0; Gaps 0

QY    1 atggccttaaaagtgtactagacaagaagaaaacgcttttccactcttttagtattacta 60
      |||||||
Db     65 atggccttaaaagtgtactagacaagaagaaaacgcttttccactcttttagtattacta 124

QY    61 ggcctatttgcatgtaaagtgaacttgtgaacacagagagactgtagacagcaagaattcagg 120
      |||||||
Db     125 ggcctatttgcatgtaaagtgaacttgtgaatcaggagactgtagacagcaagaattcagg 184

QY    121 gatcggtctggaaactgtgttccttcgcaaccagtggtggccagcatggagtggtcttaag 180
      |||||||
Db     185 gatcggtctggaaactgtgttccttcgcaaccagtggtggccagcatggagtggtcttaag 244

QY    181 gaatgtggcttcggtctatgggaggaatgcacagtggtgacgtgcccgctgcacaggttc 240
      |||||||
Db     245 gaatgtggcttcggtctatgggaggaatgcacagtggtgacgtgcccgctgcacaggttc 304

QY    241 agsgaggactggggcttcocagaaatcycaagccctgtctggactgcgcagtggtgaaccgc 300
      |||||||
Db     305 aegagagactggggcttcacagaaatgycaagccctgtctggactgcgcagtggtgaaccgc 364

```

XX V33361;
AC
XX
XX
DT 02-DEC-1998 (first entry)
XX
DE Nucleotide sequence of human alpha-OAF065.
XX
XX Human; alpha-OAF065; stroma cell; antibody; inflammatory;
KW cytokine-mediated disease; rheumatism; ulcerative colitis; ss.
XX
XX Homo sapiens.
OS
XX

FH Key Location/Qualifiers
FT CDS 45..1298
FT /*tag= a
FT /product= "human alpha-OAF065 protein"
FT sig_peptide 45..119
FT /*tag= b
FT mat_peptide 120..1295
FT /*tag= c
FT /transl_except= (pos:711..713, aa= Pro)
FT /transl_except= (pos:714..716, aa= Arg)
XX

PN WO9838304-A1.

XX 03-SEP-1998.

XX 26-FEB-1998; 98WO-JP00799.

XX 27-FEB-1997; 97JP-0043143.

XX (ONOF) ONO PHARM CO LTD.

XX Fukushima D, Konishi M, Tada H;

XX WPI: 1998-481205/41.

DR P-PSDB; W70386.

XX Membrane polypeptide expressed by human stroma cells, and antibodies
PT recognising it - for treatment of inflammatory and other
PT cytokine-mediated diseases.

XX Claim 5; Pages 31-32; 54pp; Japanese.

CC This is the nucleotide sequence of the human alpha-OAF065, used in
CC the method of the invention. The process involves the use of peptides
CC expressed by stroma cells, and its antibodies are used for in the
CC prevention and treatment of inflammatory and other cytokine-mediated
CC diseases such as rheumatism, ulcerative colitis.

XX Sequence 1704 BP; 429 A; 426 C; 430 G; 419 T; 0 other;

Query Match 98.1%; Score 1244.8; DB 19; Length 1704;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1246; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 atggctttaaagtgctactagaacaagagaaaagctttttcactcttttagtattacta 60
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
45 atggctttaaagtgctactagaacaagagaaaagctttttcactcttttagtattacta 104
QY 61 ggcattttgctatgataaagtgtgtgaacacaggagactgtagacagcaagaatttcagg 120
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
105 ggcattttgctatgataaagtgtgtgaacacaggagactgtagacagcaagaatttcagg 164
QY 121 gatcgctcggaaactgtgttcctcgtcaaccagtgctggccagggaatgagttgtctaag 180
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
165 gatcgctcggaaactgtgttcctcgtcaaccagtgctggccagggaatgagttgtctaag 224
QY 181 gaatgtgctcggctatgggagaggtgcacagtgtgtacgtgccgctgcacaggttc 240
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
225 gaatgtgctcggctatgggagaggtgcacagtgtgtacgtgccgctgcacaggttc 284

RESULT 5

X24978

ID X24978 standard; cDNA; 2185 BP.

XX

QY 241 aaggaggactgggcttcacagaaatgcaagccctgtctggactgcgcagtggtgaaccgc 300
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
285 aaggaggactgggcttcacagaaatgcaagccctgtctggactgcgcagtggtgaaccgc 344
QY 301 ttctagaaggcaaatgtttcagccaccagtgatgcattcgtcggggactgcttgcagga 360
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
345 ttctagaaggcaaatgtttcagccaccagtgatgcattcgtcggggactgcttgcagga 404
QY 361 ttctatagaagacaaaactgtcggcttcaagacatgagatgtcctctgtgagagac 420
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
405 ttctatagaagacaaaactgtcggcttcaagacatgagatgtcctctgtgagagac 464
QY 421 cctctcctcttaagcaaccgcaactgtgcaagcaaggtcaacctcgtgaagatcgctcc 480
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
465 cctctcctcttaagcaaccgcaactgtgcaagcaaggtcaacctcgtgaagatcgctcc 524
QY 481 acggctccagcccaacgggaacacggcgtggtgcgttatctcagcgctctgcaccac 540
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
525 acggctccagcccaacgggaacacggcgtggtgcgttatctcagcgctctgcaccac 584
QY 541 gtctgtggtccctgctcctcctcctcctcctcctcctcctcctcctcctcctcctc 600
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
585 gtctgtggtccctgctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 644
QY 601 aaaccacagctgctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 660
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
645 aaaccacagctgctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 704
QY 661 cttgacagactcagctccacgaatatgccacagagcctcgtcagtcgcgcgtgac 720
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
705 cttgacagactcagctccacgaatatgccacagagcctcgtcagtcgcgcgtgac 764
QY 721 tcagtcagacacctgcggccggtgcgttgcctccatccatgcctgtgagagagcctgc 780
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
765 tcagtcagacacctgcggccggtgcgttgcctccatccatgcctgtgagagagcctgc 824
QY 781 agccccaacccgcgactcttgggtggtggtgcattctgcagcagctcttcacagcaaga 840
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
825 agccccaacccgcgactcttgggtggtggtgcattctgcagcagctcttcacagcaaga 884
QY 841 aacgcagggccacgggggagatggtgcgaactttctcctcagtcacacagtcacac 900
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
885 aacgcagggccacgggggagatggtgcgaactttctcctcagtcacacagtcacac 944
QY 901 tgtggcagttttcagatgcctgcctcctgctgagcagaatcccatgggtggtgacacac 960
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
945 tgtggcagttttcagatgcctgcctcctgctgagcagaatcccatgggtggtgacacac 1004
QY 961 tcttttctgactcttctcctgaactcactggagagacattcattctcctcattccagaa 1020
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1005 tcttttctgactcttctcctgaactcactggagagacattcattctcctcattccagaa 1064
QY 1021 cttgaaagctcaacgtctcttggattcaaatagcagtcgaagatttgggtgggctgtt 1080
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1065 cttgaaagctcaacgtctcttggattcaaatagcagtcgaagatttgggtgggctgtt 1124
QY 1081 ccagtcacgtctcattctgaaacactttacagcagctcactgatttattctagataaacaac 1140
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1125 ccagtcacgtctcattctgaaacactttacagcagctcactgatttattctagataaacaac 1184
QY 1141 acactggtgaatcagcatcaactcaggatgcactaaactatgagaagccagctagatcag 1200
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1185 acactggtgaatcagcatcaactcaggatgcactaaactatgagaagccagctagatcag 1244
QY 1201 gagagtggcgtctatcctcaccacagccactcagacgtccctccaggta 1248
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1245 gagagtggcgtctatcctcaccacagccactcagacgtccctccaggta 1292

AC X24978;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE Human TRAIN-R cDNA.
 XX
 KW TRAIN-R; receptor; human; tumour necrosis factor receptor;
 KW agonist; antagonist; cancer; immunological disease; therapy;
 KW cytostatic; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 179..1432
 FT CDS /*tag= a
 FT sig_peptide 179..253
 FT /*tag= b
 FT mat_peptide 254..1429
 FT /*tag= c
 XX
 PN WO9913078-A1.
 XX
 PD 18-MAR-1999.
 XX
 PF 11-SEP-1998; 98WO-US19030.
 XX
 PR 06-MAY-1998; 98US-0084422.
 PR 12-SEP-1997; 97US-0058631.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Hession C, Tschopp J;
 XX
 XX WPI: 1999-229238/19.
 DR P-PSDB; W98146.
 XX
 PT New cysteine-rich tumor necrosis factor receptor
 XX
 PS Claim 1; Page 27; 30pp; English.
 XX
 CC The present sequence encodes a novel human cysteine-rich tumour
 CC necrosis factor receptor family member termed TRAIN-R (see W98146).
 CC It is a composite of 2 overlapping lambda gt10 clones (GJ159 and
 CC GJ158) from a Clontech human adult lung cDNA library. Human
 CC TRAIN-R was also cloned from a second sequence subclone of a
 CC lambda gt10 cDNA (GJ156, see X24979). Human TRAIN-R is expressed
 CC at low levels in every tissue and cell line tested thus far, with
 CC higher expression detected in heart, prostate, ovary, testis,
 CC peripheral blood lymphocytes, thyroid and adrenal gland.
 CC Cell death can be induced by administering an agent capable of
 CC inhibiting the binding of TRAIN-R to its ligand. A claimed method
 CC of treating, or reducing, the advancement, severity or effects of
 CC an immunological disease in a mammal comprises administering a
 CC pharmaceutical composition which comprises a TRAIN-R blocking agent,
 CC e.g. soluble TRAIN-R. TRAIN-R can be fused to an immunoglobulin to
 CC produce a fusion protein which may be targeted to various sites.
 CC It can be used in binding assays, and to identify antagonists and
 CC agonists. Anti-TRAIN-R antibodies can be used to reduce the
 CC severity of an immune response or to treat cancer. TRAIN-R
 CC blocking agents can also be used to reduce the severity or effects
 CC of an immunological disease (all claimed).
 XX
 SQ Sequence 2185 BP; 546 A; 551 C; 550 G; 538 T; 0 other;

Query Match 97.7%; Score 1240; DB 20; Length 2185;
 Best Local Similarity 99.6%; Pred. NO. 0;
 Matches 1243; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 0;
 QY 1 atggctttaaagtctactagacaagagaaaaacgttttttactcttttagtattacta 60
 DB 179 atggctttaaagtctactagacaagagaaaaacgttttttactcttttagtattacta 238

QY 61 ggctattgtcatgttaagtgaactgtgtaaacagaggagactgtagacagcaaatccagg 120
 DB 239 ggctattgtcatgttaagtgaactgtgtaaacagaggagactgtagacagcaaatccagg 298
 QY 121 gatcggctcggaaaactgtgttccctgcacacacagtggtggccaggcattgagttgtctaaag 180
 DB 299 gatcggctcggaaaactgtgttccctgcacacacagtggtggccaggcattgagttgtctaaag 358
 QY 181 gaatgtggtctcggctatggtggagagatcacagtggtgacgtgcccgtgcacaggttc 240
 DB 359 gaatgtggtctcggctatggtggagagatcacagtggtgacgtgcccgtgcacaggttc 418
 QY 241 aaggaggactggggtccagaaaatcgaagccctgtctggaactgagcagtggtggaaccgc 300
 DB 419 aaggaggactggggtccagaaaatcgaagccctgtctggaactgagcagtggtggaaccgc 478
 QY 301 ttccagaagcgaatgtgtccagccacagtgatgccatctgcgggactgcttgccagga 360
 DB 479 ttccagaagcgaatgtgtccagccacagtgatgccatctgcgggactgcttgccagga 538
 QY 361 ttttatagaagacgaactgtcggctttcaagacatgagtggtgctgctgtgagagac 420
 DB 539 ttttatagaagacgaactgtcggctttcaagacatgagtggtgctgctgtgagagac 598
 QY 421 cctcctcctcttacgaacgcgactgtgccagcaaggtcaacctgtgaagatcgcgctcc 480
 DB 599 cctcctcctcttacgaacgcgactgtgccagcaaggtcaacctgtgaagatcgcgctcc 658
 QY 481 acggctccagcccccagggacacggcgctggctggcttattctgcagcgctctggccacc 540
 DB 659 acggctccagcccccagggacacggcgctggctggcttattctgcagcgctctggccacc 718
 QY 541 gtcctgtggcctgctcactcctctgtcactatattgaagagacagtttatggagaag 600
 DB 719 gtcctgtggcctgctcactcctctgtcactatattgaagagacagtttatggagaag 778
 QY 601 aaaccagctggtctctgcggtcacagagacattcagatacaacggctctgagctgctgtgt 660
 DB 779 aaaccagctggtctctgcggtcacagagacattcagatacaacggctctgagctgctgtgt 838
 QY 661 cttagacagacctcagctccacgaatatgccacagagacctgtctgcagtcgcgcctgac 720
 DB 839 tttagacagacctcagctccacgaatatgccacagagacctgtctgcagtcgcgcctgac 898
 QY 721 tcagtcacacactgcggccggctgcttgcctccatccatgctgtgagagagcctgc 780
 DB 899 tcagtcacacactgcggccggctgcttgcctccatccatgctgtgagagagcctgc 958
 QY 781 agcccaacccggcgactcttgggtgtgggtgcatcttcgagccagctcttcaggcaaga 840
 DB 959 agcccaacccggcgactcttgggtgtgggtgcatcttcgagccagctcttcaggcaaga 1018
 QY 841 aacgcggcccccagccgggagatggtgcgcgactttcttggatccctcagcagtcacac 900
 DB 1019 aacgcggcccccagccgggagatggtgcgcgactttcttggatccctcagcagtcacac 1078
 QY 901 tgtggcgagtttcagatgcctgcctctgagtcagaatcccatgggtggtgacacacac 960
 DB 1079 tgtggcgagtttcagatgcctgcctctgagtcagaatcccatgggtggtgacacacac 1138
 QY 961 tcttttttgactcttctatcctgaactcactggagagacattctctctcaatccagaa 1020
 DB 1139 tcttttttgactcttctatcctgaactcactggagagacattctctctcaatccagaa 1198
 QY 1021 cttgaaagctcaacgtcttttgattcaaatagcagtcagagatttgggtggggtgtgt 1080
 DB 1199 cttgaaagctcaacgtcttttgattcaaatagcagtcagagatttgggtggggtgtgt 1258
 QY 1081 ccagtcagctctcattctctcaaaacttcacagcagctactgatttctctagatatacaac 1140
 DB 1259 ccagtcagctctcattctctcaaaacttcacagcagctactgatttctctagatatacaac 1318
 QY 1141 acactggtgagatcagcatcaactcaggatgcactaactatgagaagccagctagatcag 1200

```

Db 1319 acatggttagaatcagcatcaactcaggatgcactaactatgagaagccagctagatcag 1378
QY 1201 gagagtgcgctatcatccaccagccactcagcagctccctccaggtta 1248
Db 1379 gagagtgcgctgctatccaccagccactcagcagctccctccaggtta 1426

RESULT 6
X59346
ID X59346 standard; cDNA; 987 BP.
AC X59346;
XX
XX
DT 20-SEP-1999 (first entry)
DE Human NTR-5 cDNA.
XX
KW NTR-5; human; receptor; signal transduction; bone; muscle;
KW diagnosis; therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT sig_peptide 1..57
FT /*tag= a
FT mat_peptide 58..987
FT /*tag= b
XX
PN W09933967-A2.
XX
XX 08-JUL-1999.
XX
XX 28-DEC-1998; 98WO-US27688.
XX
XX 29-DEC-1997; 97US-0068925.
XX
XX (REGE-) REGENERON PHARM INC.
XX
XX Valenzuela DM;
XX
XX WPI; 1999-419102/35..
XX P-PSDB; Y06400.
XX
XX New mammalian receptor NTR-5 polypeptides
XX Claim 2a; Page 21-22; 27pp; English.
XX
XX This is the claimed coding region of human cDNA encoding a novel
XX receptor, designated NTR-5 (see Y06400), that shows homology to
XX osteoprotegerin and tumour necrosis factor receptor. The cDNA was
XX isolated from a heart cDNA library using mouse NTR-5 cDNA (see
XX X59345) as probe. Homology to osteoprotegerin suggests that NTR-5
XX is involved in the regulation of bone mass, and may be useful for
XX regulating development, proliferation and death of osteoblast or
XX osteoclast cells or for regulating muscle metabolism, and that it
XX may be implicated in muscle diseases or disorders. A host-vector
XX system for production of NTR-5 is claimed. NTR-5 polypeptides can
XX be used as immunogens and in screening assays to identify NTR-5
XX ligands, agonists and antagonists. The NTR-5 polynucleotide is
XX useful as a diagnostic tool, and as a source of probes and primers.
XX The invention also provides for diagnostic and therapeutic methods
XX based on the interaction of NTR-5 and agents that initiate signal
XX transduction through binding to NTR-5.
XX
XX Sequence 987 BP; 220 A; 251 C; 278 G; 238 T; 0 other;

Query Match 65.8%; Score 835.6; DB 20; Length 987;
Best Local Similarity 99.5%; Pred. No. 7.1e-247;
Matches 838; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 atggccttaaaagtctactagaacaagagaaaacgtttttcactcttttagtattacta 60

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Db 1 atggccttaaaagtctactagaacaagagaaaacgtttttcactcttttagtattacta 60
QY 61 ggctatttgtcatgtaaaagtgaactgtgaaacacagagagactgtagacagcaagaattcagg 120
Db 61 ggctatttgtcatgtaaaagtgaactgtgaaacacagagagactgtagacagcaagaattcagg 120
QY 121 gatcggtctgaaactgtgttccctgcaacacagtggtggccagcagcatggaattgtcctaag 180
Db 121 gatcggtctgaaactgtgttccctgcaacacagtggtggccagcagcatggaattgtcctaag 180
QY 181 gaatgtggtctcggtatggtgggagagatgcacagtgtgtgacgtgccggtcacaggttc 240
Db 181 gaatgtggtctcggtatggtgggagagatgcacagtgtgtgacgtgccggtcacaggttc 240
QY 241 aaggagactggggtctccagaaaatgaagccctgtgtgagctgccgactgcgaagtgtgaaccgc 300
Db 241 aaggagactggggtctccagaaaatgaagccctgtgtgagctgccgactgcgaagtgtgaaccgc 300
QY 301 ttccagaagcacaattgttcagccaccagtgtgccatctgcgggactgcttgcacaga 360
Db 301 ttccagaagcacaattgttcagccaccagtgtgccatctgcgggactgcttgcacaga 360
QY 361 tttataggaagacgaactgttcggcttttcaagacatggagtggtgtgccttggagac 420
Db 361 tttataggaagacgaactgttcggcttttcaagacatggagtggtgtgccttggagac 420
QY 421 cctcctcctcttaagaaacgcacgtgtgcagaaaggtcaacctcgtgaaagatcgctcc 480
Db 421 cctcctcctcttaagaaacgcacgtgtgcagaaaggtcaacctcgtgaaagatcgctcc 480
QY 481 acggcctccagccacacgggacacggcgtgctgccgttatctcagcgcctctgcccacc 540
Db 481 acggcctccagccacacgggacacggcgtgctgccgttatctcagcgcctctgcccacc 540
QY 541 gtccctgtggccctgtcctcctctgtgtcatttattgttaagagacagtttatggagaag 600
Db 541 gtccctgtggccctgtcctcctctgtgtcatttattgttaagagacagtttatggagaag 600
QY 601 aaaccacagctgtctctcgttcaggaacattcagatacaaacggctctgagctgctgt 660
Db 601 aaaccacagctgtctctcgttcaggaacattcagatacaaacggctctgagctgctgt 660
QY 661 ctgacagacctcagctccacgaatatgccacagagcctgtgccagtcgcgcgtgac 720
Db 661 ttgacagacctcagctccacgaatatgccacagagcctgtgccagtcgcgcgtgac 720
QY 721 tcagtgcagacctcggggccgggtgctgttccatccatccatctgtgtgagagagcctg 780
Db 721 tcagtgcagacctcggggccgggtgctgttccatccatccatctgtgtgagagagcctg 780
QY 781 agccccaacccggcagctcttgggtgtgggtgcatctcagcagctctcagcagcaaga 840
Db 781 agccccaacccggcagctcttgggtgtgggtgcatctcagcagctctcagcagcaaga 840
QY 841 aa 842
Db 841 aa 842

RESULT 7
X23413
ID X23413 standard; DNA; 1678 BP.
XX
XX X23413;
AC
XX
XX 18-JUN-1999 (first entry)
DT
DE Mouse mAP04-alpha (long) DNA.
XX
XX Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW developmental abnormality; gestational abnormality; prostate cancer;
KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW

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X23414
ID X23414 standard; DNA; 886 BP.
XX
AC X23414;
XX
DT 18-JUN-1999 (first entry)
XX
DE Mouse mAPO4-alpha (short) DNA.
XX
KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW developmental abnormality; gestational abnormality; prostate cancer;
KW APO6; APO8; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW apoptosis; mouse; mAPO4-alpha; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
CDS 72..716
FT /*tag= a
FT /product= "mAPO4-alpha short"
XX
PN W09911791-A2.
XX
PD 11-MAR-1999.
XX
PF 04-SEP-1998; 98WO-US18393.
XX
PR 05-SEP-1997; 97US-0924634.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Chaudhary PM;
XX
PT WPI: 1999-205191/17.
DR P-PSDB; W93580.
XX
PT New Tumor Necrosis Factor family receptor polypeptides and ligands -
PT useful for diagnosis and treatment of prostate cancer and
PT developmental or gestational abnormalities
XX
PS Example IV; Fig 7B; 156pp; English.
XX
CC This invention describes isolated Tumor Necrosis Factor (TNF) family
CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC their active fragments. APO4 is useful for diagnosing prostate cancer
CC by determining levels of APO4 in an individual. Prostate cancer can also
CC be treated using APO4 selective binding agents linked to a therapeutic
CC moiety. APO4 polypeptides are also useful for identifying selective
CC binding agents, useful in diagnosis/treatment of disease by binding of
CC agents to the polypeptide/active fragment which is extracellular, or
CC expressed on the cell surface. The binding is preferably performed in
CC vivo. APO4 polypeptides/active fragments are also useful for screening
CC for agonists and antagonists by binding and observing the change in APO4
CC activity. Effective pharmacological agents useful in diagnosis or
CC treatment of disease are also identified using APO4 polypeptides/active
CC fragments and APO4 signal transducer molecules that specifically interact
CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC activity. The method is performed in vivo or in vitro. APO polypeptides
CC are all useful as immunogens for preparing antibodies. APO4 is also
CC useful for diagnosis/treatment of developmental or gestational
CC abnormalities. APO8 was transfected to human breast carcinoma cell line
CC MCF-7, and induced apoptosis.
XX
SQ Sequence 886 BP; 204 A; 245 C; 247 G; 190 T; 0 other;

Query Match 35.4%; Score 449; DB 20; Length 886;
Best Local Similarity 82.4%; Pred. NO. 4.9e-128;
Matches 515; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
QY 1 atggttttaaaagtctactagaacaagaaagcgtttttcactcttttagtattacta 60

Db	72	atggcaactcaaggtctcctacctctacacagcggtgctcttcgctgccattctctocta	131
Qy	61	ggctattgtcatgtaaagtactgtgaacacagagagacttagacacagaagaattcagg	120
Db	132	ctccacctggcatgtaaaagtgtgcaaacccgagattgcagcgacgaggaattcaag	191
Qy	121	gatcggtctgaaactgtgtccctgcacacagtggtggccagcgcatggagtgtctaag	180
Db	192	gatcatgtgaaactgtgtccctgcacacagtggtggccagcgcatggagtgtccaag	251
Qy	181	gaatgtgcttcggtatgggagatgcacagtggtgacgtgcccgtgcacaggttc	240
Db	252	gaatgtgcttcggtatgggagatgcacagtggtgacgtgcccgtgcacaggttc	311
Qy	241	aaggagagctgggctctccagaaatgaaagccctgtctggactgcgagtggtgaacgc	300
Db	312	aaggagagctgggctctccagaaatgaaagccctgtctggactgcgagtggtgaacgc	371
Qy	301	tttcagaaggcaaatgttcagccaccagtgatgcacatctgcgggagctgcttgcagga	360
Db	372	tttcagaaggcaaatgttcagccaccagtgatgcacatctgcgggagctgcttgcagga	431
Qy	361	ttttataggaagacgaactgtcggttttcaagacatggagtggtgcttctgtggagac	420
Db	432	ttttaccggaagacaaactgtgttttcaagacatggagtggtgcttctgtggagac	491
Qy	421	ctctctctcttaccgaacccagctgtgccagcaaggtcaacctgtgaagatcgctcc	480
Db	492	ccacctctctctacgaacccagctgtgccagcaaggtcaacctgtgaagatcgctcc	551
Qy	481	acggcctccagccacgggacacggcgtgctgcgttatctgcagcgctctgcccacc	540
Db	552	accgtctccagccctcgggacacggcgtgctgcgttatctgcagcgctctgcccacc	611
Qy	541	gtcctgtggtcctgtcctcctctgtgtcatctatttgaagacagagtttatggagaag	600
Db	612	gtgctgtcgcctgtcctcctctgtgtcatctactcaagagcgagttcatggagaag	671
Qy	601	aaaccacagctgtctctggtgtcac	625
Db	672	aaaccacagctgtgaagctccatccc	696

RESULT 9
X24977
ID X24977 standard; CDNA; 942 BP.
XX
AC X24977;
XX
DT 05-JUL-1999 (first entry)
XX
DE Mouse TRAIN-R (long form) CDNA.
XX
KW TRAIN-R; receptor; mouse; tumour necrosis factor receptor;
KW agonist; antagonist; cancer; immunological disease; therapy;
KW cytosolic; ss.
OS Mus musculus.
FH Key Location/Qualifiers
CDS 101..745
FT /*tag= a
XX
PN W09913078-A1.
XX
PD 18-MAR-1999.
XX
PF 11-SEP-1998; 98WO-US19030.
XX
PR 06-MAY-1998; 98US-0084422.
PR 12-SEP-1997; 97US-0058631.
XX

Best Local Similarity 82.1%; Pred. NO. / .4e-124;
Matches 513; Conservative 0; Mismatches 111; Indels 1; Gaps 1;

QY 1 atggctttaaaagtgtactactagacaagaacgtttttcactctcttttagtacta 60
 DB 55 atggcactcaaggtctactactacacagacggtgtctctctgctccattctccta 114
 QY 61 ggtatttgcataagtgacttggtaaacaggagactgtagacagcaagaattcagg 120
 DB 115 ctccactggcatgtaagtgagtgagtgacacggagattgcaggcagggaattcaag 174
 QY 121 gatcgcttggaacgtgttccctccaaccagtggtggccaggcaatggattgctaag 180
 DB 175 gatcgatcggaaactgtctctctcaaacagtcggacctggcagtgagttgtccaag 234
 QY 181 gaattgtgcttgcctatggggaggatgcacagtggtgacgtgcccgtgcacaggttc 240
 DB 235 gaattgtgcttgcctatggggaggatgcacagtggtgacgtgcccgtgcacaggttc 294
 QY 241 aaggagactggggcttccagaataacgaagccctgtctggaactgcagtggtgaaccgc 300
 DB 295 aaggagactggggcttccagaataacgaagccctgtctggaactgcagtggtgaaccgc 354
 QY 301 ttccagaagcaaatgttccagccaccagtgatgccatctgcgggactgtgcccaggga 360
 DB 355 ttccagaagcaaatgttccagccaccagtgatgccatctgcgggactgtgcccaggga 414
 QY 361 ttctataggaagcaaatgttccagccaccagtgatgccatctgcgggactgtgcccaggga 420
 DB 415 ttctataggaagcaaatgttccagccaccagtgatgccatctgcgggactgtgcccaggga 474
 QY 421 cctctctctcttaccagaacgcactgtgcccagcaagtgcaacctctgtgaagatcgctcc 480
 DB 475 ccactctctcttaccagaacgcactgtgcccagcaagtgcaacctctgtgaagatcgctcc 534
 QY 481 acggctctccagccagggacacggcgctgctgccttatctgacgcctctggccacc 540
 DB 535 acggctctccagccagggacacggcgctgctgccttatctgacgcctctggccacc 594
 QY 541 gtctgtggtcctgtctcactctctgtctgtctatctattgtaagagacagttatggagaag 600
 DB 595 gtctgtcctg-cctgtctcactctgtgtctatctactactgcaagaggcagttcaggagaag 653
 QY 601 aaaccagctgtctctgsggtcac 625
 DB 654 aaaccagctgtgaagctccatccc 678

RESULT 12

XD X59345
 AC X59345 standard; cDNA; 538 BP.
 XX
 AC X59345;
 XX
 DT 20-SEP-1999 (first entry)
 XX
 DE Mouse NTR-5 cDNA.
 XX
 KW NTR-5; mouse; receptor; signal transduction; bone; muscle;
 KW diagnosis; therapy; ss.
 XX
 OS Mus musculus.
 XX
 FT Key Location/Qualifiers
 FT CDS 3..485
 FT /*tag= a
 XX
 PN W09933967-A2.
 XX
 PD 08-JUL-1999.
 XX
 XX 28-DEC-1998; 98WO-US27688.
 XX
 XX 29-DEC-1997; 97US-0068925.
 XX

PA (REG-) REGENERON PHARM INC.
 XX
 PI Valenzuela DM;
 XX
 DR WPI; 1999-419102/35.
 DR P-PSDB; Y06399.
 XX
 PT New mammalian receptor NTR-5 polypeptides
 XX
 XX Example 1; Page 19; 27pp; English.
 XX
 CC This is the nucleotide sequence of murine cDNA coding for a novel
 CC receptor, designated NTR-5 (see Y06399), that shows homology to
 CC osteoprotegerin and tumor necrosis factor (TNF) receptor. 2 cDNA
 CC clones containing the present sequence were isolated following an
 CC EST database search using human and mouse TNF family members as
 CC query sequences. The murine NTR-5 cDNA was used as a probe in
 CC the isolation of human NTR-5 cDNA (see X59346). Homology to
 CC osteoprotegerin suggests that NTR-5 is involved in the regulation
 CC of bone mass, and may be useful for regulating development,
 CC proliferation and death of osteoblast or osteoclast cells or for
 CC regulating muscle metabolism, and that it may be implicated in
 CC muscle diseases or disorders. A host-vector system for production
 CC of NTR-5 is claimed. NTR-5 polypeptides can be used as immunogens
 CC and in screening assays to identify NTR-5 ligands, agonists and
 CC antagonists. The NTR-5 polynucleotide is useful as a diagnostic
 CC tool, and as a source of probes and primers. The invention also
 CC provides for diagnostic and therapeutic methods based on the
 CC interaction of NTR-5 and agents that initiate signal transduction
 CC through binding to NTR-5.
 XX
 SQ Sequence 538 BP; 111 A; 153 C; 152 G; 122 T; 0 other;

Query Match 28.6%; Score 362.6; DB 20; Length 538;
 Best Local Similarity 86.2%; Pred. No. 1.3e-101;
 Matches 401; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
 QY 161 caggcagtgagttgtcctaaggaatgtggtctcgctatggaggaggtcacagtgtgta 220
 DB 1 ctggcagtgagttgtcctaaggaatgtggtctcgctatggaggaggtcacagtgtgta 60
 QY 221 cgtgcggctgcacaggttcaaggagactggggtctccagaaatgcaagccctgtctg 280
 DB 61 cctgcaggcgcgacccgttcaaggagactggggtctccagaaatgcaagccctgtctg 120
 QY 281 actgcgagtggtgaaccgctttcagaaggaactgttcagccaccagtgatgccatct 340
 DB 121 actgtgcgtggtgaaccgctttcagaaggaactgttcagccaccagtgatgccatct 180
 QY 341 gcggggactgcttgcagagcttctctctctctctctcagaaactgtcgtcttcaagacatg 400
 DB 181 gcggggactgcttgcagagcttctctctctctctcagaaactgtcgtcttcaagacatg 240
 QY 401 agtgtgtgcttgcagagcttctctctctctctcagaaactgtcgtcttcaagacatg 460
 DB 241 agtgtgtgcttgcagagcttctctctctctcagaaactgtcgtcttcaagacatg 300
 QY 461 acctgtgaagatcgcgctcaagcgttccagccacgggacacggcgctggtgctgta 520
 DB 301 acctgtgaagatctctctcagcgttccagccacgggacacggcgctggtgctgta 360
 QY 521 tctgagcgtctgcccacgctctctgctgctgctgctgctgctgctgctgctgta 580
 DB 361 tctgagcgtctgcccacgctctctgctgctgctgctgctgctgctgctgctgta 420
 QY 581 agagacagtttatggagaagaacccagctggtctctcggtgtac 625
 DB 421 agagcagttcatggagaagaacccagctggttaagctccatccc 465

RESULT 13
 V11422

101 V11422 standard; cDNA; 371 BP.
102 V11422;
103 23-JUL-1998 (first entry)
104 Human secreted protein clone AX92_3 cDNA 5'-end.
105 Secreted protein; prevention; treatment; gene therapy; ds.
106 Homo sapiens.
107 W09801554-A2.
108 15-JAN-1998.
109 07-JUL-1997; 97WO-US11876.
110 09-JUL-1996; 96US-0677231.
111 (GEMY) GENETICS INST INC.
112 Bowman M, Evans C, Jacobs K, Lavallie ER, McCoy JM;
113 Merberg D, Racie LA, Spaulding V, Treacy M;
114 WPI; 1998-110230/10.
115 P-PSDB; W58844.
116 Secreted proteins and polynucleotides encoding them - useful to
117 prevent, treat and ameliorate medical conditions
118 Claim 15; Page 57; 93pp; English.
119 V11422-V11424 encode fragments of a novel secreted protein derived from
120 clone AX92_3 which was isolated from a human adult testes cDNA library.
121 The protein can be used to prevent, treat or ameliorate a medical
122 condition, while the polynucleotides can be used for gene therapy.
123 Sequence 371 BP; 83 A; 96 C; 107 G; 82 T; 3 other;
124
125 Query Match 28.5%; Score 361.6; DB 19; Length 371;
126 Best Local Similarity 98.1%; Pred. NO. 2.2e-101;
127 Matches 364; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
128
129 OY 128 ctggaaactgtgttccctgcacacagtggtggccagcatgagtggtcttaaggaaatgtg 187
130 1 ctggaaactgtgttccctgcacacagtggtggccagcatgagtggtcttaaggaaatgtg 60
131
132 OY 188 gtttcggctatgggagagatgcacagtggtgacgtgccggtgcacaggttcaaggagg 247
133 61 gtttcggctatgggagagatgcacagtggtgacgtgccggtgcacaggttcaaggagg 120
134
135 OY 248 actggggttcagaatacgaagccctgtctgaactgcgcaagtgtgaaccgtttcaga 307
136 121 actggggttcagaatacgaagccctgtctgaactgcgcaagtgtgtgaaccgtttcaga 180
137
138 OY 308 agggcaattgttcagccacagtgatgccatctgcgggactgcttgccaggaatttata 367
139 181 agggcaattgttcagccacagtgatgccatctgcgggactgcttgccaggaatttata 240
140
141 OY 368 ggaagacgaaactgttcgggtttcaagacatgagtggtgcttgtggagacctcttc 427
142 241 ggaagacgaaactgttcgggtttcaaaacatgagtggtgcttgtggagacctcttc 300
143
144 OY 428 ctccctacgaacgcactgtgcacgaaggtcaacctgtggaagatcggtccacggcct 487
145 301 ctccctacgaacgcactgtgcacgaaggtcaacctgtggaagatcggtccacggcct 360
146
147 OY 488 ccagccacgg 498
148 361 ccagccacgg 371

RESULT 14

123417
X23417 standard; DNA; 591 BP.
X23417;
18-JUN-1999 (first entry)
Mouse mAPO4-gamma DNA.
Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
developmental abnormality; gestational abnormality; prostate cancer;
APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
apoptosis; mouse; APO4-gamma; ss.
Mus sp.
Key Location/Qualifiers
CDS 95..547
FT /*tag= a
FT /product= "mAPO4-gamma"
X23417-1791-A2.
11-MAR-1999.
04-SEP-1998; 98WO-US18393.
05-SEP-1997; 97US-0924634.
(UNIW) UNIV WASHINGTON.
Chaudhary PM;
WPI; 1999-205191/17.
P-PSDB; W93583.
New Tumor Necrosis Factor family receptor polypeptides and ligands -
useful for diagnosis and treatment of prostate cancer and
developmental or gestational abnormalities
Disclosure; Fig 7E; 156pp; English.
This invention describes isolated Tumor Necrosis Factor (TNF) family
receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
their active fragments. APO4 is useful for diagnosing prostate cancer
by determining levels of APO4 in an individual. Prostate cancer can also
be treated using APO4 selective binding agents linked to a therapeutic
moiety. APO4 polypeptides are also useful for identifying selective
binding agents, useful in diagnosis/treatment of disease by binding of
agents to the polypeptide/active fragment which is extracellular, or
expressed on the cell surface. The binding is preferably performed in
vivo. APO4 polypeptides/ active fragments are also useful for screening
for agonists and antagonists by binding and observing the change in APO4
activity. Effective pharmacological agents useful in diagnosis or
treatment of disease are also identified using APO4 polypeptides/active
fragments and APO4 signal transducer molecules that specifically interact
with a cytoplasmic domain of APO4 and detecting a change in level of APO4
activity. The method is performed in vivo or in vitro. APO polypeptides
are all useful as immunogens for preparing antibodies. APO4 is also
useful for diagnosis/treatment of developmental or gestational
abnormalities. APO8 was transfected to human breast carcinoma cell line
MCF-7, and induced apoptosis.
Sequence 591 BP; 148 A; 145 C; 175 G; 123 T; 0 other;

Query Match 24.7%; Score 314; DB 20; Length 591;
Best Local Similarity 78.9%; Pred. No. 1.2e-86;
Matches 374; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 1 atggctttaaaagtctactagacaagaacgctttttcactcttttagtattacta 60
Dbb 95 atggcactcaagctctactctacacagcagtgctctctctcctcctcctccta 154
QY 61 ggcatttgcataagtgactcttgaaacaggagactgtagacagcaagaattcagg 120
Dbb 155 ctccactggcagtgtaagtgagttgcgaacccggagattgcaggcaggaattcagg 214
QY 121 gatcgtctggaacgtgttccctgcacacacagtggtggccaggcagtggttctaag 180
Dbb 215 gatcgtatctggaacgtgttccctgcacacacagtggtggccaggcagtggttctaag 274
QY 181 gatatgtgctctgctctggtgagtgacagtggtgacgtggtgacgtggtgacgtggt 240
Dbb 275 gaatgtgctctgctctggtgagtgacagtggtgacgtggtgacgtggtgacgtggt 334
QY 241 aaggagactggggtctccagaatacgaagcctgtctgagactgagtgagtgagtgag 300
Dbb 335 aaggagactggggtctccagaatacgaagcctgtgagactgagtgagtgagtgagtgag 394
QY 301 ttccagaagcgaattgttccagccaccagtgatgctctgctggtgagtgagtgagtgag 360
Dbb 395 ttccagaagcgaattgttccagccaccagtgatgctctgctggtgagtgagtgagtgag 454
QY 361 ttctatagggaagcgaattgttccagccaccagtgatgctctgctggtgagtgagtgag 420
Dbb 455 ttctatagggaagcgaattgttccagccaccagtgatgctctgctggtgagtgagtgag 514
QY 421 cctcctcctcttaccgaacgcagctgtgcccagcaagtgcaacctctgtaagatc 474
Dbb 515 ccacctcctccttaccgaacgcagctgtgcccagcaagtgcaacctctgtaagatc 568

RESULT 15

X24976
ID X24976 standard; cDNA; 599 BP.
AC X24976;
XX
XX
DT 05-JUL-1999 (first entry)
DE Mouse TRAIN-R (short form) cDNA.
XX
XX
KW TRAIN-R; receptor; mouse; tumor necrosis factor receptor;
KW agonist; antagonist; cancer; immunological disease; therapy;
KW cytostatic; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 104..556
FT /*tag= a
XX
PN W09913078-A1.
XX
PD 18-MAR-1999.
XX
PF 11-SEP-1998; 98WO-US19030.
XX
PR 06-MAY-1998; 98US-0084422.
PR 12-SEP-1997; 97US-0058631.
XX
XX (BIOJ) BIOGEN INC.
XX
PI Hession C, Tschopp J;
XX
XX WPI; 1999-229238/19.
DR P-PSDB; W98144.
XX
XX New cysteine-rich tumor necrosis factor receptor
XX
PS Claim 1; Page 26; 30pp; English.

XX The present sequence encodes a novel murine cysteine-rich tumour
CC necrosis factor receptor family member termed TRAIN-R (short form)
CC (see W98144). This putative natural soluble form of murine TRAIN-R
CC may inhibit signalling by the full-length TRAIN-R (see W98145).
CC Murine TRAIN-R is expressed at high levels in brain and lung, and
CC at lower levels in liver, skeletal muscle and kidney. Cell death
CC can be induced by administering an agent capable of inhibiting the
CC binding of TRAIN-R to its ligand. A claimed method of treating, or
CC reducing, the advancement, severity or effects of an immunological
CC disease in a mammal comprises administering a pharmaceutical
CC composition which comprises a TRAIN-R blocking agent, e.g. soluble
CC TRAIN-R. TRAIN-R can be fused to an immunoglobulin molecule to
CC produce a fusion protein which may be targeted to various sites.
CC It can be used in binding assays, and to identify antagonists and
CC agonists. Anti-TRAIN-R receptor antibodies can be used to reduce the
CC severity of an immune response or to treat cancer. TRAIN-R
CC blocking agents can be used to reduce the severity or effects of an
CC immunological disease (all claimed).
XX
SQ Sequence 599 BP; 149 A; 147 C; 180 G; 123 T; 0 other;

Query Match 24.7%; Score 314; DB 20; Length 599;
Best Local Similarity 78.9%; Pred. No. 1.3e-86;
Matches 374; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 1 atggctttaaaagtctactagacaagaagaaacgtttttcactcttttagtattacta 60
Dbb 104 atggcactcaagtgctctactctacacagcagtgctctctcctcctcctccta 163
QY 61 ggcatttgcataagtgactcttgaaacaggagactgtagacagcaagaattcagg 120
Dbb 164 ctccactggcagtgtaagtgagttgcgaacccggagattgcaggcaggaattcagg 223
QY 121 gatcgtctggaacgtgttccctgcacacacagtggtggccaggcagtggttctaag 180
Dbb 224 gatcgtatctggaacgtgttccctgcacacacagtggtggccaggcagtggttctaag 283
QY 181 gaatgtgctctgctctggtgagtgacagtggtgacgtggtgacgtggtgacgtggt 240
Dbb 284 gaatgtgctctgctctggtgagtgacagtggtgacgtggtgacgtggtgacgtggt 343
QY 241 aaggagactggggtctccagaatacgaagcctgtctgagactgagtgagtgagtgag 300
Dbb 344 aaggagactggggtctccagaatacgaagtgatgagcagtggtgagtgagtgagtgag 403
QY 301 ttccagaagcgaattgttccagccaccagtgatgctctgctggtgagtgagtgagtgag 360
Dbb 404 ttccagaagcgaattgttccagccaccagtgatgctctgctggtgagtgagtgagtgag 463
QY 361 ttctatagggaagcgaattgttccagccaccagtgatgctctgctggtgagtgagtgag 420
Dbb 464 ttctatagggaagcgaattgttccagccaccagtgatgctctgctggtgagtgagtgag 523
QY 421 cctcctcctccttaccgaacgcagctgtgcccagcaagtgcaacctctgtaagatc 474
Dbb 524 ccacctcctccttaccgaacgcagctgtgcccagcaagtgcaacctctgtaagatc 577

Search completed: March 2, 2001, 12:42:41
Job time: 31615 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 09:59:02 ; Search time 4027.99 Seconds
(without alignments)
2207.677 Million cell updates/sec

Title: US-09-380-276A-5

Perfect score: 1269

Sequence: 1 atgctttaaaagtctact.....ggcagcgactgggtccctg 1269

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

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- 2: gb_est2.*
- 3: gb_est3.*
- 4: gb_est4.*
- 5: gb_est5.*
- 6: gb_est6.*
- 7: gb_est7.*
- 8: gb_est8.*
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- 13: gb_est13.*
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190: gb_gss25:*
 191: gb_gss26:*
 192: gb_gss27:*
 193: gb_gss28:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	302.2	23.8	395	106	BE306459 601103459
2	296.4	23.4	454	147	W56629 zd16a11.r1
3	274.8	21.7	282	28	AL036000 DKFp3584K
4	241.2	19.0	534	135	BE757704 212225 MA
5	203	16.0	401	1	AA003356 mg49g01.r
6	192.8	15.2	369	91	AA478317 19558 MAR
7	174.8	13.8	358	1	AA036247 m17a03.r
8	157.6	12.4	258	133	BB542020 BB542020
9	155	12.2	643	159	AQ563354 HS_5335_B
10	125.8	9.9	646	159	AQ544065 RFCI-11-3
11	124.4	9.8	275	31	AV111112 AV111112
12	120.8	9.5	404	8	AA495217 fa04d10.r
13	113.8	9.0	450	158	AQ514075 HS_5184_A
14	95	7.5	1110	193	CNS0507C
15	91.2	7.2	414	91	AW527025 UI-R-B01-
16	80.2	6.3	381	21	AI551729 vfl1e02.y
17	67.4	5.3	442	109	BE554624 ur48c11.y
18	59	4.6	405	150	AQ173919 HS_3204_A
19	42.6	3.4	443	11	AA759377 ah54a10.s
20	41.4	3.3	551	12	AA814296 nz07d08.s
21	39.4	3.1	397	13	AA860208 ak48c10.s
22	39.4	3.1	266	128	BB350382 W47341 zc34h02.s1
23	39.2	3.1	266	128	BB350382 BB350382
24	39	3.1	407	146	W32428 zc05c12.s1
25	39	3.1	559	3	AA161105 zc05c05.s
26	38.8	3.1	706	109	BE535395 601058548
27	38.8	3.1	925	190	CNS0091P
28	38	3.0	391	21	AI522266 t18af06.x
29	38	3.0	597	97	AW968349 EST380424
30	37.8	3.0	458	88	AA303441 xv19b01.x
31	37.8	3.0	482	139	BF018062 u495a06.x
32	37.6	3.0	510	29	AU060928 AU060928
33	37.4	2.9	319	103	BB219800 BB219800
34	37.4	2.9	343	96	AW877284 MR4-PT005
35	37.4	2.9	472	7	AA417295 zu18c03.s
36	37.4	2.9	968	193	CNS056T4
37	37.4	2.9	1002	191	CNS0206F
38	37.2	2.9	344	37	AV630854
39	37.2	2.9	372	89	AW312781 5078 MARC
40	37	2.9	910	190	CNS0060N
41	36.8	2.9	366	8	AA542636 fa08d10.r
42	36.8	2.9	447	17	AI217695 qh26d07.x
43	36.8	2.9	465	38	AAQ015051 UI-H-B10-
44	36.8	2.9	465	87	AW181919 xj68d07.x
45	36.8	2.9	689	109	BE532858 601234740

ALIGNMENTS

RESULT	1	BE306459	601103459F1	NCI_CGAP_Lu29	Mus musculus	cdna	clone IMAGE:3495566	5'	13-JUL-2000
LOCUS		BE306459	395	bp	mRNA				
DEFINITION		BE306459	395	bp	mRNA				
ACCESSION		BE306459							
VERSION		BE306459.1							
KEYWORDS		EST.							
SOURCE		house mouse							

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 395)
AUTHORS NIH-MGC <http://www.ncbi.nlm.nih.gov/MGC/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Tel.: (301) 496-1550
 Email: Robert_Strausberg@nih.gov
 Tissue procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM8546 row: f column: 15
 High quality sequence stop: 395.

FEATURES
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 /strain="C57BL/6J (f1)"
 /db_xref="taxon:10090"
 /clone="IMAGE:3495566"
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 /tissue_type="spontaneous tumor, metastatic to mammary."
 Stem cell origin.
 /lab_host="DH10B"
 /note="Organ: lung; Vector: pCMV-Sport6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: oligo dt.
 Library constructed by Life Technologies. Investigator
 providing samples: Gilbert Smith, NIH"

88 a 101 c 120 g 86 t
BASE COUNT
ORIGIN

Query Match 23.8%; Score 302.2; DB 106; Length 395;
 Best Local Similarity 85.3%; Pred. No. 2.8e-78;
 Matches 337; Conservative 0; Mismatches 58; Indels 0; Gaps 0

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 Db 61 TCAAGGATCGATCTGGAACTGTGTCTCTGTCGAAACAGTGGCGACCTGGCATGGAGTTGT 120
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 QY 356 caggattttataggacgcaaaactgttcgctttcagaacatgagatgtgtgcctgtg 415
 Db 301 CAGGATTTTACCGGAGACCAAACTGGTTGGTTTTCAAGACATGGAGTGTGCCCCTCGC 360
 QY 416 gagacctctctctcttacgaaccgactgtgc 450
 Db 361 GAGACCCACTCTCTCCCTACGAACACACACTGTACC 395

RESULT 2

W56629

LOCUS

up mRNA

TSE

15-OCT-1996

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Db 241 TGTCTCATCCACCGCAGCTCAGACGTCCTCCAGGTAAAGCAGGACTGGTTCCCTG 298
|||||
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AL036000 282 bp mRNA EST 29-FEB-2000.
LOCUS DKFp564K1022.r1.564 (synonym: hfr2) Homo sapiens cDNA clone
DEFINITION DKFp564K1022.5', mRNA sequence.
ACCESSION AL036000
VERSION AL036000.1 GI:5405629
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 282)
AUTHORS Wambutt,R., Heubner,D., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Wambutt, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: Wambutt R
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
SI sequence also available.
This clone (DKFp564K1022) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="DKFp564K1022"
/clone_lib="564 (synonym: hfr2)"
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/lab_host="Xl-2blue"
/Note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"
BASE COUNT 57 a 85 c 75 g 63 t 2 others
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Best Local Similarity 98.6%; Pred. No. 3.1e-70;
Matches 276; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 425 ctctctcttacgaacccgactgtgcagcaaggtcaacctcgtgaagatcgctccacgg 484
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QY 485 cctccagccacgggacagggcgctgtgcgtgcgttctctgcagcgtctgcacccgtcc 544
|||||
Db 123 CTCCAGCCACACGGGACAGGGCGCTGGCTGCCGCTTATCTATCAGCAGCTCTGGCCACGGTCC 182
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RESULT 4
BE757704

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LOCUS BE757704 534 bp mRNA EST 15-SEP-2000
DEFINITION 212225 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE757704
VERSION BE757704.1 GI:10171696
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 534)
AUTHORS Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
,W.W. and Keeler,J.W.
TITLE Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRIMERS
FORWARD: AGGAACACAGCTATGACCAT
BACKWARD: GTTTCCTCCAGTCACGAGC
Plate: 65 row: C column: 2
Seq primer: ATTTAGGTGACACTATAG.
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/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/Note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from testis, thymus,
semitendinosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
BASE COUNT 122 a 117 c 171 g 124 t
ORIGIN
Query Match 19.0%; Score 241.2; DB 135; Length 534;
Best Local Similarity 83.6%; Pred. No. 3.4e-60;
Matches 286; Conservative 0; Mismatches 53; Indels 3; Gaps 1;
QY -1 atggctttaaaagtgtctactagaacaagagaaaacgttttctactcttttagttacta 60
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Db 196 ATGGCTTTCAACAGCTGTACTCAGGCAACAGAAA---TCCTTCACGGTTGTAGTTTACTA 252
|||||
QY 61 ggctatttctcgttaaaagtgtgaaacagggagactgtgaaacaggaactgtagacgaagaattcagg 120
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Db 253 GCCTGTTGGCATGTGGAGTGATTGTGAACAGGAGAGACTGTGCAGCAGCAGGAATTTCAGG 312
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QY 121 gatcgtctggaacctgtgttccctgcacaccagtgtyggccaggcgatggagttgtctaaag 180
|||||
Db 313 GACCACATGGAAGCTGTGTCTGTGCAAGCAGCTGTGGCCAGGCATGGAGTTGTCCAAG 372
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QY 181 gaatgtggttcgttcgtatgggagagatgcacagtgtgtacgtgcggtgcacaggttc 240
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Db 373 GAATGTGGCTTTGGCTTACGGGAGGACGCCCACTGTGTGAAGTGTGGCGCGCACAGGTTTC 432
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QY 241 aaggaggactggggcttcagaaaaatgcagccctgtctggaactgcgcagtggtgaaccgc 300
|||||
Db 433 AAGGAGGACTGGGCTCTCAGAAGTGCAGACCGCTGCCTGGACTGCGCCCTGTGTGAGCCGC 492
|||||
QY 301 ttccagaagcaaatgttcagccaccagtgatgccatctgc 342
|||||
Db 493 TTCCAGAAGGCCAACTGCTCGGCCACTGGCCACTGGCGACGCGCTGCG 534
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RESULT 5
AA003356 401 bp mRNA EST 19-JUL-1996
LOCUS mg49901.r1 Soares mouse embryo NBME13.5 14.5 Mus musculus cDNA
DEFINITION clone IMAGE:427152 5', mRNA sequence.
ACCESSION AA003356
VERSION AA003356.1 GI:1446796
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 401)
Maier, S., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:261704
Seq primer: ETPRimer
High quality sequence stop: 345.
FEATURES
Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:427152"
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/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/note="vector: p7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGCGGAAATTTTTTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru KO, Wayne
State Univ., from 2 l; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
p7T3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo."
BASE COUNT 92 a 96 c 128 g 85 t
ORIGIN

Query Match 16.0%; Score 203; DB 1; Length 401;
Best Local Similarity 78.8%; Pred. No. 6e-49;
Matches 242; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 1 atgggttttaaaagtctactagaacaaagaaaacggtttttcaactcttttagtattacta: 60
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Db 95 ATGGCACTCAAGTCTACCTTACACAGGAGCGGTCCTTCGCTGCCATCTCTCTCCTA 154
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Qy 61 ggcatttgcatgtaaagtactgtgaacacagagagactgtagacagcaagaatttcagg 120
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Db 155 CTCACCTGGCATGTAAAGTGAAGTTCGGAACCGGAGATTCAGGACGACGAGGAAATTCAG 214
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Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999).
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES

Location/Qualifiers
 1. .258
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone_lib="RIKEN full-length enriched, 0 day neonate eyeball"
 /tissue_type="eyeball"
 /dev_stage="0 day neonate"
 /lab_host="DH10B"
 /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
 GAGAGAGAGCGGCCCAACTCGAGTGTGTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
 GAGAGAGAGATTCGAGTGAATTAATATCCGCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
 55 a 77 C 66 g 60 t

BASE COUNT
 ORIGIN

Query Match 12.4%; Score 157.6; DB 133; Length 258;
 Best Local Similarity 80.7%; Pred. No. 1.4e-35;
 Matches 184; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
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 Qy 281 actgcgagtgtaaccgcttcagaaaggcaaatgttcagccacagtgatgccatc 340
 Db 61 ACTTTGCCGTGGTGNACCGCTTTAGAGGCCCACTGCTCACACCACTGATGCTTTT 120
 Qy 341 gcggggactgttgcagagatttataggaagacgaactgtcggtttcaagacatgg 400
 Db 121 GCGGGAGTGCCTGCCAGATTTTACCGGAAGACCAAACTGGTTGGTTTCAAGACATGG 180
 Qy 401 agtgtgtcctgtgagaccctcctcctcctcctcctcctcctcctcctcctcctg 448
 Db 181 AGTGTGTCCTCCGCGGAGACCACTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTG 228

RESULT 9

AQ563354
 LOCUS AQ563354 643 bp DNA GSS 29-MAY-1999
 DEFINITION HS_5335_B2_B03_77A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=911 Col=6 Row=D, DNA sequence.
 ACCESSION AQ563354
 VERSION AQ563354.1 GI:4922825
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 643)
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

TITLE

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
 99380589

MEDLINE

Contact: Mahairas GG, Wallace JC, Hood L

COMMENT

High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering.bac.htm>) or from Research Genetics (info@resgen.com). BAC end Web Server: <http://www.htsc.washington.edu>
 Plate: 911 row: D column: 6
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 643.

FEATURES

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 /sex="male"
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 151 a 154 c 158 g 167 t 13 others

BASE COUNT
 ORIGIN

Query Match 12.2%; Score 155; DB 159; Length 643;
 Best Local Similarity 85.9%; Pred. No. 1.1e-34;
 Matches 170; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
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 Db 315 TGTGCCAAGGTCACCTCGTGAAGATCGGTNACAGGGCTCCAGCCACGGGACAGC 374
 Qy 505 gcgtggtgcggttatctgcagcgctctggccaccgctcctgctgctcctcctcctc 564
 Db 375 GCGCTGTGCTGCCGTATCTGCAGCGCTCTGCCACCGCTCTGCTGCTCATCTC 434
 Qy 565 tgtgtcatctattgtaagagacagtttatgagagaacccacagctgtctctcggtca 624
 Db 435 TGTGTCTCTATTGTAGAGACAGTATGAGAGAACCCAGCTGTGAAGTGTGAGCT 494
 Qy 625 caggacattcagtaaac 642
 Db 495 CATTACATNTCTTATCAC 512

RESULT 10

AQ544065
 LOCUS AQ544065 646 bp DNA GSS 19-MAY-1999
 DEFINITION RPCI-11-315F10.TV RPCI-11 Homo sapiens genomic clone RPCI-11-315F10
 ACCESSION AQ544065
 VERSION AQ544065.1 GI:4869459
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 646)
 AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.

Search completed: March 2, 2001, 09:59:07
Job time: 28932 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 12:33:04 ; Search time 217.59 Seconds
(without alignments)
939.898 Million cell updates/sec

Title: US-09-380-276A-5
Perfect score: 1269
Sequence: 1 atggtttaaagtctact.....ggcagcgactgggtccctg 1269

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 280836 seqs, 80580151 residues
Total number of hits satisfying chosen parameters: 561672

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36.4	2.9	1601	1 US-08-722-001-7	Sequence 7, Appli
2	36.4	2.9	1987	1 US-08-722-001-26	Sequence 26, Appl
3	36.4	2.9	1997	1 US-08-722-001-27	Sequence 27, Appl
4	36.4	2.9	2004	1 US-08-722-001-11	Sequence 11, Appl
5	36.2	2.9	2485	1 US-08-424-424B-1	Sequence 1, Appli
6	36.2	2.9	2486	4 PCT-US94-05363A-1	Sequence 1, Appli
7	34.8	2.7	1639	1 US-08-334-698-5	Sequence 5, Appli
8	34.8	2.7	1639	1 US-08-228-932-5	Sequence 5, Appli
9	34.8	2.7	1639	1 US-08-468-939-5	Sequence 5, Appli
10	34.8	2.7	1639	2 US-08-406-855A-5	Sequence 5, Appli
11	34.8	2.7	1639	2 US-08-722-190-5	Sequence 5, Appli
12	34.8	2.7	1639	3 US-08-244-354-5	Sequence 5, Appli
13	34.8	2.7	1639	3 US-09-206-899-5	Sequence 5, Appli
14	34.8	2.7	1639	4 PCT-US95-04203-5	Sequence 5, Appli
15	34.6	2.7	5962	5 5386025-5	Patent No. 5386025
16	34.6	2.7	7218	1 US-08-232-463-14	Sequence 14, Appl
17	33.6	2.6	800	2 US-08-416-603-11	Sequence 11, Appl
18	33.4	2.6	4360	1 US-08-470-350B-1	Sequence 1, Appli
19	33	2.6	9472	1 US-08-325-547-9	Sequence 9, Appli
20	32.8	2.6	2230	1 US-08-200-512-1	Sequence 1, Appli
21	32.6	2.6	1593	2 US-08-524-828-2	Sequence 2, Appli
22	32.6	2.6	1593	2 US-08-975-114A-2	Sequence 2, Appli
23	32.6	2.6	1593	3 US-08-849-281A-2	Sequence 2, Appli
24	32.6	2.6	2247	2 US-08-524-828-1	Sequence 1, Appli
25	32.6	2.6	2247	2 US-08-975-114A-1	Sequence 1, Appli
26	32.6	2.6	3891	1 US-08-480-604A-27	Sequence 27, Appl
27	32.6	2.6	3891	2 US-08-405-496A-27	Sequence 27, Appl
28	32.4	2.6	1167	1 US-07-960-985-1	Sequence 1, Appli

29	32.4	2.6	1167	2 US-08-496-671-1	Sequence 1, Appli
30	32.4	2.6	1690	2 US-08-461-812-3	Sequence 3, Appli
31	32.4	2.6	3083	2 US-08-480-994-36	Sequence 36, Appl
32	32.4	2.6	3083	2 US-08-616-844-36	Sequence 36, Appl
33	32.4	2.6	3083	2 US-08-599-654-36	Sequence 36, Appl
34	32.4	2.6	3083	2 US-08-485-573-36	Sequence 36, Appl
35	32.4	2.6	3083	3 US-08-944-868A-36	Sequence 36, Appl
36	32.4	2.6	3083	3 US-08-944-423A-36	Sequence 36, Appl
37	32.4	2.6	3083	3 US-08-925-743-36	Sequence 36, Appl
38	32.4	2.6	3083	3 US-08-944-496-36	Sequence 36, Appl
39	32.4	2.6	3084	3 US-08-826-246-11	Sequence 11, Appl
40	32.4	2.6	3084	3 US-08-944-495-11	Sequence 11, Appl
41	32.4	2.6	3084	3 US-09-126-640-6	Sequence 6, Appli
42	32.4	2.6	28804	2 US-08-592-874-1	Sequence 1, Appli
43	32.4	2.6	28804	3 US-09-096-942-2	Sequence 2, Appli
44	32.4	2.6	28804	3 US-09-096-867-2	Sequence 2, Appli
45	32.2	2.5	953	1 US-08-197-793-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-722-001-7
; Sequence 7, Application US/08722001
; Patent No. 5760054
; GENERAL INFORMATION:
; APPLICANT: Thompson, Wayne J.
; APPLICANT: Huff, Joel R.
; APPLICANT: Nerenberg, Jennie B.
; APPLICANT: Lee, Hee-Yoon
; APPLICANT: Bell, Ian M.
; TITLE OF INVENTION: ALPHAIc ADRENERGIC RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07065

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,001
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,276
FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Appollina, Mary A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19169Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3462
TELEFAX: (908)594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1601 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-722-001-7

Db 1166 GGGCTCTTCTACCGCTCTTGGCCATCATCTGCTGATCTAGTACGCGGCTACGTGCT 1225

QY 594 ggagagaacacccagctgtctcgcggtc 623

Db 1226 GCGCAAGAGGAGAGCGGGGCTCAAGTC 1255

RESULT 4

US-08-722-001-11
; Sequence 11, Application US/08722001
; Patent No. 5760054
; GENERAL INFORMATION:
; APPLICANT: Thompson, Wayne J.
; APPLICANT: Huff, Joel R.
; APPLICANT: Nerenberg, Jennie B.
; APPLICANT: Lee, Hee-Yoon
; APPLICANT: Bell, Ian M.
; TITLE OF INVENTION: ALPHALIC ADRENERGIC RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07065

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,001
; FILING DATE:

CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/229,276
; FILING DATE: 14-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Appollina, Mary A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19169Y
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; TELEX: 138825

INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2004 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-722-001-11

Query Match 2.9%; Score 36.4; DB 1; Length 2004;

Best Local Similarity 52.7%; Pred. No. 0.21; Mismatches 0; Indels 0; Gaps 0;

QY 474 cgcgtccagcgcctccagccacggagacgcgtgggtccgttatctgcagcgctct 533

Db 1107 CGAGGACGAGACCATCTGCCAGATCAACGAGGCGCGGCTAGTCTCTTCTCGGCTCT 1166

QY 534 ggcacccgtctgtgcccctgcctcatcctctgtgtcatctattgttaagagacagtttat 593

Db 1167 GGGCTCTTCTACCTGCTGCGCATCATCTGCTGCTAGTCTAGTCTGCGGCTACGTGCT 1226

QY 594 ggagagaacacccagctgtctcgcggtc 623

Db 1227 GCGCAAGAGGAGAGCGGGGCTCAAGTC 1256

RESULT 5

US-08-424-424B-1
; Sequence 1, Application US/08424424B
; Patent No. 5759854
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Neurotransmitter Transporter
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,424B
; FILING DATE: APRIL 21, 1995
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05363
; FILING DATE: MAY 25, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-308

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2485 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
US-08-424-424B-1

Query Match 2.9%; Score 36.2; DB 1; Length 2485;

Best Local Similarity 56.2%; Pred. No. 0.28; Mismatches 0; Indels 0; Gaps 0;

QY 453 caaggtcaacgtcgtaagatcgctccagcgctccagccacggagacacggcgctgac 512

Db 2023 CAGCATCATCCAGCTGGGGGTACGCCGCCCTACAGCGCTTGGATCAAGGAGAGGC 2082

QY 513 tgccgttatctgcagcgctctgtggccacgcctctgtggccctgctcatctctgtgtcat 572

Db 2083 TGCCGAGCGCTACCTGTATTTCCCAACTGGCCCATGGCACCTCTCATCACCTCATCGT 2142

QY 573 c 573

Db 2143 C 2143

RESULT 6

PCT-US94-05363A-1
; Sequence 1, Application PC/TUS9405363A
; GENERAL INFORMATION:

; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Neurotransmitter Transporter
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/334,698
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA: APPLICATION NUMBER: US/07/952,798
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 376901
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: (212) 422523 COOP UI
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1639 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 126..1523
OTHER INFORMATION:
-334-698-5

Query Match 2.7%; Score 34.8; DB 1; Length 1639;
Best Local Similarity 52.0%; Pred. No. 0.59;
Matches 78; Conservative 0; Mismatches 72; Indels 0

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OQy		
dDb		
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OQy		
dDb		
534	ggcacgcgtcgtcgtggccctgcatactctgtgtcatctatctgaagagacagtttat	593
OQy		
dDb		
695	GGGTCTCTTTACTGCTGCCTTGCCCATCATCTGGTCATACTGTAACCCCGCTACSTGGT	754
OQy		
594	ggagaagaaaccagctggttctctgcggtc	623
OQy		
dDb		
755	GGCCACAGGAGAGAGCGGGGGCTCAAGTC	784

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RESULT      8
US-08-228-932-5
; Sequence 5, Application US/08228932
; Patent No. 5578611
; GENERAL INFORMATION:
; APPLICANT: Charles Gluchowski, Carlos C. Forray, George Chlu,
; APPLICANT: Theresa A. Brancheh, John M. Wetzel and Paul R. Hartig
; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN
; TITLE OF INVENTION: PROSTATIC HYPERPLASIA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,932
; FILING DATE: 13-APR-1994

```

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878-B/JPW/TEP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: (212) 422523 COOP UI
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1639 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 126..1523
OTHER INFORMATION:
US-08-228-932-5

Query Match 2.7%; Score 34.8; DB 1; Length 1639;
Best Local Similarity 52.0%; Pred. No. 0.59;
Matches 78; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 474 cgcgtccacggcctccagcccaaggacagcgctggtcgctgtatctgagcgctct 533
DB 635 CGAGGACGAGACCATCTGCCAGATCAACGAGGAGCGGGCTACGTCTTCTCAGCGCT 694
QY 534 ggcacccgtcctgtgcccctctcatctctgtgtcattctattgtaagagacagttat 593
DB 695 GGGCTCTTCTACCTGCGCTCTGGCCATCATCTGCTGCTACTGCTGCTGCTGCTGCT 754
QY 594 ggaagaagaacccagctggtctctcggtc 623
DB 755 GGCCAAGAGGAGAGCGGGGCTCAAGTC 784

RESULT 9
US-08-468-939-5
Sequence 5, Application US/08468939
Patent No. 5714381
GENERAL INFORMATION:
APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,939
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41337-1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1639 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 126..1523
OTHER INFORMATION:
US-08-468-939-5

Query Match 2.7%; Score 34.8; DB 1; Length 1639;
Best Local Similarity 52.0%; Pred. No. 0.59;
Matches 78; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 474 cgcgtccacggcctccagcccaaggacagcgctggtcgctgtatctgagcgctct 533
DB 635 CGAGGACGAGACCATCTGCCAGATCAACGAGGAGCGGGCTACGTCTTCTCAGCGCT 694
QY 534 ggcacccgtcctgtgcccctctcatctctgtgtcattctattgtaagagacagttat 593
DB 695 GGGCTCTTCTACCTGCGCTCTGGCCATCATCTGCTGCTACTGCTGCTGCTGCTGCT 754
QY 594 ggaagaagaacccagctggtctctcggtc 623
DB 755 GGCCAAGAGGAGAGCGGGGCTCAAGTC 784

RESULT 10
US-08-406-855A-5
Sequence 5, Application US/08406855A
Patent No. 5861309
GENERAL INFORMATION:
APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,855A
FILING DATE: 21-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KDB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1639 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)

US-08-722-190-5

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Best Local Similarity	52.0%;	Pred. No. 0.59;		
Matches 78;	Conservative 0;	Mismatches 72;	Indels 0;	Gaps 0;

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Qy	534	ggccaccgtctgctggccctgctcaccctctgtgctatctattgtaagagacagtttat	593
Db	695	GGGCTCTTCTTACCTGCTCTGGCCATCATCTGGTCATGTACTGCCGCGTCTACGTGGT	754
Qy	594	ggagaagaacccccagctggctctgctgggtc	623
Db	755	GGCCAAGAGGGAGAGCGGGGCTCAAAGTC	784

RESULT 12
US-08-244-354-5
: Sequence 5, Application US/08244354
: Patent NO. 6015819

REFERENCE: CHARLES SCHROEDER, JR.
 TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
 TREAT BENIGN PROSTATIC HYPERPLASIA
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: COOPER & DUNHAM LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.24
 CURRENT APPLICATION DATA:

FILING DATE: April 1, 1997
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 41878-D-PCT-US/JPW
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-0525
 TELEX:
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1639 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown

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; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 126..1523
; OTHER INFORMATION:
;
US-08-244-354-5

Query Match 2.7%; Score 34.8; DB 3; Length 1639;
Best Local Similarity 52.0%; Pred. No. 0.59;
Matches 78; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

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1

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 1118133 seqs, 6853842396 residues

Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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84: gb_htg24:*
85: gb_pr8:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	823	48.3	1678	11	AF167552	AF167552	Mus muscu
5	692.6	40.6	1075	11	AF173166	AF173166	Mus muscu
6	460.8	27.0	744	11	AB040433	AB040433	Mus muscu
7	460.8	27.0	886	11	AF167553	AF167553	Mus muscu
8	420.2	24.7	143608	67	AL161422	AL161422	Homo sapi
9	420.2	24.7	178256	66	AL139080	AL139080	Homo sapi
10	326.6	19.2	591	11	AF167554	AF167554	Mus muscu
c 11	73	4.3	188351	67	AL353136	AL353136	Homo sapi
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c 13	65.4	3.8	205736	51	AC033560	AC033560	Homo sapi
c 14	43.6	2.6	160214	54	AC034198	AC034198	Homo sapi
c 15	43.6	2.6	180511	42	AC018836	AC018836	Homo sapi
c 16	43.6	2.6	209876	10	AC011599	AC011599	Homo sapi
c 17	42.6	2.5	98218	59	AC074232	AC074232	Oryza sat
c 18	42.6	2.5	196312	42	AC006616	AC006616	Mus muscu
c 19	42	2.5	207166	42	AC018843	AC018843	Homo sapi
c 20	41.4	2.4	147001	68	AL355986	AL355986	Homo sapi
c 21	41.2	2.4	186797	49	AC021965	AC021965	Homo sapi

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c 22 40.2 2.4 217422 59 AC073747 AC073747 Mus muscu
23 40.2 2.4 236195 59 AC073713 AC073713 Mus muscu
24 39.2 2.3 178715 68 AL359536 AL359536 Homo sapi
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27 38.8 2.3 204573 41 AC016589 AC016589 Homo sapi
28 38.4 2.3 145934 67 AL353611 AL353611 Homo sapi
29 38.4 2.3 148018 67 AL159992 AL159992 Homo sapi
30 38.4 2.3 171491 50 AC022606 AC022606 Homo sapi
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32 38.4 2.3 259474 78 HUAC004605 AC004605 Homo sapi
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35 38 2.2 166704 70 AP001559 AP001559 Homo sapi
36 38 2.2 189199 9 AC006566 AC006566 Homo sapi
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42 37.6 2.2 189841 57 AC068802 AC068802 Homo sapi
43 37.4 2.2 32354 73 SCD84 AL353816 Streptomy
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45 37.2 2.2 128200 84 CNS01DMN AL137785 Homo sapi

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ALIGNMENTS

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LOCUS Homo sapiens mRNA for hTROY, complete cds.
ACCESSION AB040434
VERSION AB040434.1 GI:9392329
SOURCE hTROY.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites) Morikawa, Y., Copeland, N.G., Gilbert, D.J., Jenkins, N.A.,
AUTHORS Senba, E. and Kitamura, T.
TITLE TROY, a newly identified member of the tumor necrosis factor
receptor superfamily, exhibits a homology with Edar and is
expressed in embryonic skin and hair follicles
J. Biol. Chem. 275 (27), 20742-20747 (2000)
JOURNAL 20347167
MEDLINE 2 (bases 1 to 1364)
REFERENCE Kojima, T. and Kitamura, T.
AUTHORS Kojima, T. and Kitamura, T.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-2000) to the DDBJ/EMBL/GenBank databases, Tetsuo
Kojima, Chugai Research Institute for Molecular Medicine, Inc.,
Cytochrome Research Program; 153-2 Nagai, Niihari, Ibaraki 300-4101,
Japan (E-mail: kojima@cimmed.com, Tel:81-298-306211,
Fax:81-298-306270)
COMMENT Sequence updated (06-Apr-2000).
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Source Location/Qualifiers
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37..1308
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Best Local Similarity 99.7%; Pred. No. 0;
Matches 1280; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Db 1 AGAACTCTCCAAACAATAATACATTTTGTATAAGAAAGATGCTTTAAAACTGCTACTAGAA 60
QY 69 caagagaagaacgtttttcactctcttttagtattactagggtatttgcattgtaaaagtact 128
Db 61 CAAGAGAAACAGTCTTTTCACTCTCTTTTAGTATTACTTAGGCTATTGTGTCATGTAAGTGACT 120
QY 129 tgtgaacacaggagactgtagacagcaagaattcagagatcggtctgagaactgtgttccc 188
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QY 609 tgtgcatctattgtaagagacagtttatggagaagaacccacgctgggtctctgaggtca 668
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QY 669 caggacatcagtcacacgctcgtgactgtgtgtcttgacagacctcagctccacgaa 728
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Db 961 CCTCTGATGCGAAGTCCCATGGGTGGTGACAAACATCTCTTTTGTGACTCTTATCCTGAA 1020
Qy 1029 ctcaatgagagacattcattctctcaatccagaaacttgaaagctcaacgtcttttgat 1088
Db 1021 CTCACGTGAGAGACATTCATTTCTCTCAATCCAGAACTTGAAGCTCAACGCTTTGGAT 1080
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Db 1081 TCAAAATAGCAGTCAAGATTTGGTGTGGTGGGGGTGTTCAGTCCAGCTCATCTCTGAAAC 1140
Qy 1149 ttacagcagctactgatttacttagataaacaacacactggttagaatcagcatcaact 1208
Db 1141 TTTACAGCAGCTACCTGATTTATCTAGATATACAAACACTGCTGTAAGATCAGCATCAACT 1200
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Qy 1269 gccactcagagctccctccaggaa 1292
Db 1261 GCCACTCAGACGCTCCCTCCAGGTA 1284

RESULT 2
AF167555 AF167555 1489 bp mRNA PRI 25-MAY-2000
LOCUS Homo sapiens TAJ-alpha mRNA, complete cds.
DEFINITION AF167555
ACCESSION AF167555
VERSION AF167555.1 GI:8071643
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1489)
AUTHORS Eby, M.T., Jasmin, A., Kumar, A., Sharma, K. and Chaudhary, P.M.
TITLE TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
Activates the c-Jun N-terminal Kinase Pathway and Mediates
Caspase-Independent Cell Death
J. Biol. Chem. 275 (20), 15336-15342 (2000)
10809768
REFERENCE 2 (bases 1 to 1489)
AUTHORS Chaudhary, P.M.
TITLE Direct Submission
Submitted (12-JUL-1999) Internal Medicine, UT Southwestern Medical
Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8593, USA
FEATURES
Location/Qualifiers
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Query Match

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RESULT 3

AB040432 3964 bp mRNA ROD 22-JUL-2000

LOCUS Mus musculus mRNA for TROY, complete cds.

DEFINITION AB040432

ACCESSION AB040432

VERSION AB040432.1 GI:9392325

KEYWORDS TROY.

SOURCE Mus musculus cDNA to mRNA.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Kojima,T., Morikawa,Y., Copeland,N.G., Gilbert,D.J., Jenkins,N.A., Senba,E. and Kitamura,T.

TITLE TROY, a newly identified member of the tumor necrosis factor receptor superfamily, exhibits a homology with Edar and is expressed in embryonic skin and hair follicles

JOURNAL J. Biol. Chem. 275 (27), 20742-20747 (2000)

MEDLINE 20347167

REFERENCE 2 (bases 1 to 3964)

AUTHORS Kojima,T.

TITLE Direct Submission

JOURNAL Submitted (23-MAR-2000) to the DDBJ/EMBL/GenBank databases. Tetsuo Kojima, Chugai Research Institute for Molecular Medicine, Inc., Cytokine Research Program; 153-2 Nagai, Nihari, Ibaraki 300-4101, Japan (E-mail:kojimat@climmed.com, Tel:81-298-306211, Fax:81-298-306270)

FEATURES

Location/Qualifiers

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ORIGIN

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Best Local Similarity 71.9%; Pred. No. 6.9e-219;

Matches 1195; Conservative 0; Mismatches 431; Indels 36; Gaps 7;

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Qy	1639	gcctcatgctcttcttctggtgattggttggttttacaagac	1680
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ACCESSION	AF167552		
VERSION	AF167552.1	GI:8071637	
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ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; Mus.	
REFERENCE		1 (bases 1 to 1678)	
AUTHORS		Eby M.T., Jasmin A., Kumar A., Sharma K. and Chaudhary P.M.	
TITLE		TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family, Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-independent Cell Death	
JOURNAL		J. Biol. Chem. 275 (20), 15336-15342 (2000)	
PUBLISHED		10809768	
REFERENCE		2 (bases 1 to 1678)	
AUTHORS		Chaudhary P.M.	
TITLE		Direct Submission	
JOURNAL		Submitted (12-Jul-1999) Internal Medicine, UT Southwestern Medical Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8593, USA	
FEATURES		Location/Qualifiers	
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JOURNAL	Genomics 62 (1), 103-107 (1999)
MEDLINE	20054362
REFERENCE	2 (bases 1 to 1075)
AUTHORS	Hu,S.
TITLE	Direct Submission
JOURNAL	Submitted (29-JUL-1999) Department of Immunology, Mayo Clinic and Foundation, 200 First Street SW, Rochester, MN 55905, USA
FEATURES	Location/Qualifiers
source	1..1075
CDS	/organism="Mus musculus" /db_xref="taxon:10090" 28..1074 /codon_start=1 /product="TNFRSF19" /protein_id="AAF19795.1" /db_xref="GI:6635355" /translation="MALAKVLPRLTVLFAATLLFLHLACKVSCFAGCDROEPEKDRSG NCVLCKQGPQMEISKEGCFYGEDACVPCRPHPREKEDWGFQKRCACALVNRRPQ RANCSTSDAVCGDCPLPGFYRKTLVLQFQDMCEVPCGDPDPPIYPHCITSKVNLVKSLS TVSSPHRTDLAAATVCSALATVLLALLILVLYCKRPMKPSMLRPLQDIOYNGSEL SCFDPLRHCARHACQYHRDASPMYGPVHLIPSLCCEARSARAVLGCGLRSPPT LQERNPASVGNTPAFFCGSVSRISCAEFSDAWPLMQNPPLGDDSLSDSYPELTGDTN SLNPEMLCFRFRDL"
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Db	1126 AGGATCTGGCTGGGACAGCTGCTCTAGAGCTCTCTGGGAATCTTTTCAGAACTACTGACT 1185
Qy	1162 ctgatttatctagatataacacacacactggttagaatacagcatcaactcagatgactaa 1221
Db	1186 CACCTAGACATGCTGACATGCTGACAGTCTGGGACGACGCTAGCTCAGGATGCTCAA 1245
Qy	1222 ctatgagaagccagctagatcatcgagagagtggtgctctatcatccaccacgacctcagcgt 1281
Db	1246 GGACTCCAAGCCCAAGGAGGCTGGGAGACAGAGGAAACCTGAATCTAGCCATGCCACACAG 1305
Qy	1282 cccctcagaagctttaaagaacctgcttcttctgcagttagaagcgtgtgctggaaccca 1341
Db	1306 CCTTCCAGGATGCTGAAG---GCCATCTTCTGACGCTGGAGGTGGGTCTGGACAC- 1360
Qy	1342 aagagtactccttcttagctctatgagctgagcagctctgacacctgcatggtctctggg 1401
Db	1361 -----GCCTGTGATGAGCCCTACAGACTGACAGTCTGTG-----GTGCTGGAA 1404
Qy	1402 gcaaaataaatctgaacaaactgacggcatttgaaagcctttcagccaggttgcctctga 1461
Db	1405 GCAAAATAAATCTGAACAAATGACAAACATTTTCCATCTTTCAGCCACTAGCTACTGA 1464
Qy	1462 gcagacagctctagctgaaacctcaatgaataacaaagaagaactcca----ggcgg 1517
Db	1465 GCCAGACCACTGTAGCTGAACACCCACCAAGAACAGAGAGACTGTGCTGTAGCGC 1524
Qy	1518 actcatgatactctgcatcttctcatagaaagctctctgcccacaaaagtgcactca 1577
Db	1525 GCCTTGGGACATGTGCTTCTTCCCTAAGCGAAACCTTAGCTGGGGCCA-----ATTGTA 1579
Qy	1578 aagacggatgggttgagctggcagcctatgagatttgagacataatacaagaagaacaaa 1637
Db	1580 AGGACCCATGGGTGGAATGTGCTGCTGTGAACTTGTGGGCACAGCA---GGACCCACG 1635
Qy	1638 tgcctcatgcttatttcaatggatggtgattgtggttttacaagac 1680
Db	1636 CTGGCTCTCTTATGTCACGGGTGAATGTGGTTTCACAAAGAC 1678

RESULT 5

AF173166 1075 bp mRNA ROD 26-DEC-1999

LOCUS Mus musculus TNFRSF19 mRNA, complete cds.

DEFINITION AF173166

ACCESSION AF173166

VERSION AF173166.1 GI:6635354

KEYWORDS house mouse.

SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1075)

AUTHORS Hu,S., Tamada,K., Ni,J., Vincenz,C. and Chen,L.

TITLE Characterization of TNFRSF19, a novel member of the tumor necrosis factor receptor superfamily

RESULT	8
AL161422	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
FEATURES	
source	
misc_	
misc_	
misc_	
BASE COUNT	
ORIGIN	


```
Query Match      24.7%; Score 420.2; DB 67; Length 143608;
Best Local Similarity 86.4%; Pred. No. 4.1e-105;
Matches 464; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 1168 tatctagatatacaacacactggttagaatacagatcaactcagagtgacactaactatga 1227
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 89373 TATTATTATCCATGTACTACTAGTAAAGATTATGCATATAATATCTTTTACCATTTGA 89432

Qy 1228 gaagccagctagatcagagagtgccgtatcatccaccagccagccagcagcctccc 1287
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 89433 AATTTAGCAGATTTAACTGTGAACATATTTCTTAAGCTTCCCTTCTGTGCTGTTTT 89492

Qy 1288 aggaagcttaagaacctgctcttcttcagtgagaagcgtgctggaaccccaaaagagt 1347
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 89493 AGGAAGCTTAAAGAACCTGCTTCTTCGTCAGTAGAAGCGGTGCTGGAACCCAAAGAGT 89552

Qy 1348 actcctttgttagcttagctagcagtgagcagctctggacccttcagtgctctgaggcaaaa 1407
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 89553 ACTCCTTTGTTAGGCTTATGAGCTTATGAGCTGAGCAGTCTGGACCTTGCGCTTCGGGCAAAA 89612

Qy 1408 ataaatctgaacaaactgacgcgcaattgaagcctttcagccagttgcttctctgagccaga 1467
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 89613 ATAAATCTGAACCAAACTGACGGCATTTGAAGCCTTTGAGCCAGTTGCTTCTGAGCCAGA 89672

Qy 1468 ccagctgtaagctgaacactcaatgaataacaagaagaagactccagggccgactcatgata 1527
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 89673 CCAGCTGTAAGCTGAACCTCAATGAATAAACAAGAAAGACTCCAGGCGGACTCATGATA 89732

Qy 1528 ctctgcatcttctctacatgagaagcttctctgccaaaaagtgacttcaagacggatg 1587
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 89733 CTCTGCATCTTTCTACATGAGAAGCTTCTCTGCCACAAAAGTACTTCAAGACGGATG 89792

Qy 1588 ggttgagctgacgactgatgattgtgacataatacaagaagaacagaaatgcctcatg 1647
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 89793 GGTTCAGCTGCGCCTATGAGATTGTGGACATATAACAAGAAACAGAAATGCCCTCATG 89852

Qy 1648 cttatttctcgtgattgtgttttacaagactgaagaccagagtagtatacttttc 1704
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 89853 CTTATTTCATGCTGATTGTGTTTACAAAGCTGAAGACCCAGAGTACTACTTTTTC 89909

RESULT 9
AL139080 178256 bp DNA HTG 29-SEP-2000
LOCUS Homo sapiens chromosome 13 clone RP11-173N17 map q12.11-12.3, ***
DEFINITION SEQUENCING IN PROGRESS ***, 15 unordered pieces.
ACCESSION AL139080
VERSION AL139080.8 GI:10443032
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 178256)
Direct Submission
Submitted (28-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerquest@sanger.ac.uk
On Oct 1, 2000 this sequence version replaced gi:10129398.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: ba173N17
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 168976 bases at least Q40
```

Consensus quality: 172107 bases at least Q30
Consensus quality: 173780 bases at least Q20
Insert size: 176856; sum-of-contigs
Insert size: 163577; 8.6% error; agarose-fp
Quality coverage: 3.73x in Q20 bases; sum-of-contigs Quality
coverage: 4.07x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 8223: contig of 8223 bp in length
* 8224 8323: gap of 100 bp.
* 8324 25426: contig of 17103 bp in length
* 25427 25526: gap of 100 bp
* 25527 28263: contig of 2737 bp in length
* 28264 28363: gap of 100 bp
* 28364 34273: contig of 5910 bp in length
* 34274 34373: gap of 100 bp
* 34374 42235: contig of 7862 bp in length
* 42236 42335: gap of 100 bp
* 42336 53917: contig of 11582 bp in length
* 53918 54017: gap of 100 bp
* 54018 71972: contig of 17955 bp in length
* 71973 72072: gap of 100 bp
* 72073 81711: contig of 9639 bp in length
* 81712 81811: gap of 100 bp
* 81812 88644: contig of 6833 bp in length
* 88645 88744: gap of 100 bp
* 88745 95048: contig of 6304 bp in length
* 95049 95148: gap of 100 bp
* 95149 107455: contig of 12307 bp in length
* 107456 107555: gap of 100 bp
* 107556 125465: contig of 17910 bp in length
* 125466 125565: gap of 100 bp
* 125566 140008: contig of 14443 bp in length
* 140009 140108: gap of 100 bp
* 140109 144761: contig of 4653 bp in length
* 144762 144861: gap of 100 bp
* 144862 178256: contig of 33395 bp in length.

FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="13"
/map="q12.11-12.3"
/clone="RP11-173N17"
/clone_lib="RPC1-11.1"
1..8223
/note="assembly_fragment:01724
fragment_chain:1"
8324..25426
/note="assembly_fragment:00074
fragment_chain:1"
25527..28263
/note="assembly_fragment:01884
fragment_chain:1"
28364..34273
/note="assembly_fragment:00979
fragment_chain:1"
34374..42235
/note="assembly_fragment:00126
fragment_chain:2"
42336..53917
/note="assembly_fragment:00364
fragment_chain:2"
54018..71972
/note="assembly_fragment:01769
fragment_chain:2"

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

Db 548 TGTGCCAAGTGGCAGCAGACC 568

|||||

RESULT 11

AL353136/c

LOCUS AL353136 188351 bp DNA HTG 10-AUG-2000

DEFINITION Homo sapiens chromosome X clone RP11-133K18, *** SEQUENCING IN PROGRESS ***, 16 unordered pieces.

ACCESSION AL353136

VERSION AL353136.6 GI:9796991

KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 188351)

TITLE Pavitt,R

JOURNAL Direct Submission

COMMENT Submitted (09-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Aug 12, 2000 this sequence version replaced gi:9368011.

----- Genome Center

Center: Sanger Center

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: humquery@sanger.ac.uk

----- Project Information

Center project name: BA133K18

----- Summary Statistics

Assembly program: XGAP4; version 4.5

Sequencing vector: plasmid; L08752; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Consensus quality: 176827 bases at least Q40

Consensus quality: 181768 bases at least Q30

Consensus quality: 184650 bases at least Q20

Insert size: 186851; sum-of-contigs

Insert size: 162009; 18.4% error; agarose-fp

Quality coverage: 3.49x in Q20 bases; sum-of-contigs Quality coverage: 4.02x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1 25437: contig of 25437 bp in length

* 25438 25537: gap of 100 bp

* 25538 27653: contig of 2116 bp in length

* 27654 27753: gap of 100 bp

* 27754 45836: contig of 18083 bp in length

* 45837 45936: gap of 100 bp

* 45937 58298: contig of 12362 bp in length

* 58299 58398: gap of 100 bp

* 58399 63898: contig of 5500 bp in length

* 63899 63998: gap of 100 bp

* 63999 70792: contig of 6794 bp in length

* 70793 70892: gap of 100 bp

* 70893 83402: contig of 12510 bp in length

* 83403 83502: gap of 100 bp

* 83503 112513: contig of 29011 bp in length

* 112514 112613: gap of 100 bp

* 112614 120587: contig of 7974 bp in length

* 120588 120687: gap of 100 bp

* 120688 126817: contig of 6130 bp in length

* 126818 126917: gap of 100 bp

* 126918 135398: contig of 8481 bp in length

* 135399 135498: gap of 100 bp

* 135499 149082: contig of 13584 bp in length

	* 149083	149182:	gap of	100 bp
	* 149183	157907:	contig of	8725 bp in length
	* 157908	158007:	gap of	100 bp
	* 158008	163704:	contig of	5697 bp in length
	* 163705	163804:	gap of	100 bp
	* 163805	175258:	contig of	11454 bp in length
	* 175259	175358:	gap of	100 bp
	* 175359	188351:	contig of	12993 bp in length.
FEATURES			Location/Qualifiers	
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	/db_xref="taxon:9606"			
	/chromosome="X"			
	/clone="RP11-133K18"			
	/clone_lib="RPCI-11.1"			
misc_feature	1.	25437		
	/note="assembly_fragment:01650"			
	clone_end:SP6			
	vector_side:left"			
misc_feature	25338..	27653		
	/note="assembly_fragment:00293"			
	fragment_chain:1"			
misc_feature	27754..	45836		
	/note="assembly_fragment:01209"			
	fragment_chain:1"			
misc_feature	45937..	58298		
	/note="assembly_fragment:01684"			
	fragment_chain:1"			
misc_feature	58399..	63898		
	/note="assembly_fragment:00037"			
	fragment_chain:1"			
misc_feature	63999..	70792		
	/note="assembly_fragment:01432"			
	fragment_chain:2"			
misc_feature	70893..	83402		
	/note="assembly_fragment:00471"			
	fragment_chain:2"			
misc_feature	83503..	112513		
	/note="assembly_fragment:00822"			
	fragment_chain:2"			
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	/note="assembly_fragment:00509"			
	fragment_chain:3"			
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	/note="assembly_fragment:01092"			
	fragment_chain:3"			
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	/note="assembly_fragment:00273"			
misc_feature	135499..	149082		
	/note="assembly_fragment:00291"			
misc_feature	149183..	157907		
	/note="assembly_fragment:01278"			
misc_feature	158008..	163704		
	/note="assembly_fragment:00964"			
	fragment_chain:4"			
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	/note="assembly_fragment:00415"			
	fragment_chain:4"			
misc_feature	175359..	188351		
	/note="assembly_fragment:00856"			
	fragment_chain:4"			
	clone_end:T7			
BASE COUNT	57974	a	35482	c 35967 g 57418 t 1510 others
ORIGIN				

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Query Match      4.3%; Score 73; DB 67; Length 188351;
Best Local Similarity 60.2%; Pred. No. 6.5e-09;
Matches 121; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
Qy 223 aggaatgtggcttcggtatggaggaggtcacagtgtgtcacgtgcgcggctgcacagt 282

```



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* 131074 143236: contig of 12163 bp in length
* 143237 143336: gap of 100 bp
* 143337 154478: contig of 11142 bp in length
* 154479 154578: gap of 100 bp
* 154579 169967: contig of 15389 bp in length
* 169968 170067: gap of 100 bp
* 170068 187347: contig of 17280 bp in length
* 187348 187447: gap of 100 bp
* 187448 205736: contig of 18289 bp in length.
```

FEATURES

source

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1. 205736
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
/map="17"
/clone="RP11-85120"
/clone.lib="RPC1-11 Human Male BAC"
1. .1267
/note="assembly_fragment"
1368. .2402
/note="assembly_fragment"
2503. .3524
/note="assembly_fragment"
3625. .4913
/note="assembly_fragment"
5014. .6289
/note="assembly_fragment"
6390. .7655
/note="assembly_fragment"
7756. .9267
/note="assembly_fragment"
9368. .11138
/note="assembly_fragment"
11239. .13822
/note="assembly_fragment"
13923. .18968
/note="assembly_fragment"
17069. .20185
/note="assembly_fragment"
20286. .22634
/note="assembly_fragment"
22735. .27012
/note="assembly_fragment"
27113. .29342
/note="assembly_fragment"
clone_end:T7
vector_side:right"
29443. .33381
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33482. .36562
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36663. .40982
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41083. .45520
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45621. .50623
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50724. .55610
/note="assembly_fragment"
55711. .61038
/note="assembly_fragment"
61139. .66159
/note="assembly_fragment"
66260. .73479
/note="assembly_fragment"
73580. .80554
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89414. .98132
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Query Match

4.3%; Score 73; DB 51; Length 205736;

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Best Local Similarity 60.2%; Pred. No. 6.6e-09;
Matches 121; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
QY 223 aggaatgtgcttcggctatggaggagatgcacagtgtagcgtgtagcgggtgcacaggt 282
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 79395 AGGATTGTGGTTATGGAGAGGGTGGAGATGCCTACTACACAGCCCTGCTCGCAGGT 79336
QY 283 tcaaggaggactgggcttcagaaatcaagccctgtctggactgcagtggtgaacc 342
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 79335 ACAAAGCAGCTGGGCCACACAGATGTGAGATGCATCACCTGTCTGTCTCATCATC 79276
QY 343 gcttcagaaggcaaatgttcagccaccagtgatgccatctgctggactgcctgcag 402
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 79275 GTGTTCAAGAGTCAACTGCACAGCTACCTCTAATGCTGTGTGTGGGACTGTTTGCCCA 79216
QY 403 gatattataggaacacaaac 423
Db 79215 GGTGAGCTTGCTTTATGAGAC 79195
```

RESULT 13

```
AC023560 205736 bp DNA HTG 12-MAR-2000
LOCUS Homo sapiens chromosome 17 clone RP11-85120 map 17, WORKING DRAFT
DEFINITION SEQUENCE, 34 unordered pieces.
AC023560
AC023560.2 GI:7229913
VERSION HTG: HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS human.
SOURCE Homo sapiens
```

```
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
REFERENCE 1 (bases 1 to 205736)
```

```
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
```

```
TITLE Homo sapiens chromosome 17, clone RP11-85120
```

```
JOURNAL Unpublished
```

```
REFERENCE 2 (bases 1 to 205736)
```

```
AUTHORS
```

```
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bada, F., Boguslavsky, L.,
Boukhalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
Dearellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, W.,
Fenster, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., Landers, T., Larcocque, K., Lehoczy, J., Levine, R.,
Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M.,
McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrum, J.,
Meneus, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J., Naylor, J.,
Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Ollivar, T. M.,
Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C.,
Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Tirrell, A.,
Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B.,
Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and
Zody, M.
```

```
Direct Submission
```

```
TITLE
```

```
JOURNAL
```

```
COMMENT
```

```
Submitted (15-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 12, 2000 this sequence version replaced gi:6978256.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WITB
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L6741
Center clone name: 85_I-20
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----- Summary Statistics -----
 Sequencing vector: M13; M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 178666 bases at least Q40
 Consensus quality: 190940 bases at least Q30
 Consensus quality: 197088 bases at least Q20
 Insert size: 194000; agarose-fp
 Insert size: 202436; sum-of-contigs
 Quality coverage: 4.2 in Q20 bases; agarose-fp
 Quality coverage: 4.0 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 34 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

```

1 1267: contig of 1267 bp in length
* 1268 1367: gap of 100 bp
* 1368 2402: contig of 1035 bp in length
* 2403 2502: gap of 100 bp
* 2503 3524: contig of 1022 bp in length
* 3525 3624: gap of 100 bp
* 3625 4913: contig of 1289 bp in length
* 4914 5013: gap of 100 bp
* 5014 6289: contig of 1276 bp in length
* 6290 6389: gap of 100 bp
* 6390 7655: contig of 1266 bp in length
* 7656 7755: gap of 100 bp
* 7756 9267: contig of 1512 bp in length
* 9268 9367: gap of 100 bp
* 9368 11138: contig of 1771 bp in length
* 11139 11238: gap of 100 bp
* 11239 13822: contig of 2584 bp in length
* 13823 13922: gap of 100 bp
* 13923 16968: contig of 3046 bp in length
* 16969 17068: gap of 100 bp
* 17069 20185: contig of 3117 bp in length
* 20186 20285: gap of 100 bp
* 20286 22634: contig of 2349 bp in length
* 22635 22734: gap of 100 bp
* 22735 27012: contig of 4278 bp in length
* 27013 27112: gap of 100 bp
* 27113 29342: contig of 2230 bp in length
* 29343 29442: gap of 100 bp
* 29443 33381: contig of 3939 bp in length
* 33382 33481: gap of 100 bp
* 33482 36562: contig of 3081 bp in length
* 36563 36662: gap of 100 bp
* 36663 40982: contig of 4320 bp in length
* 40983 41082: gap of 100 bp
* 41083 45520: contig of 4438 bp in length
* 45521 45620: gap of 100 bp
* 45621 50623: contig of 5003 bp in length
* 50624 50723: gap of 100 bp
* 50724 55610: contig of 4887 bp in length
* 55611 55710: gap of 100 bp
* 55711 61038: contig of 5328 bp in length
* 61039 61138: gap of 100 bp
* 61139 66159: contig of 5021 bp in length
* 66160 66259: gap of 100 bp
* 66260 73479: contig of 7220 bp in length
* 73480 73579: gap of 100 bp
* 73580 80554: contig of 6975 bp in length
* 80555 80654: gap of 100 bp
* 80655 89313: contig of 8659 bp in length
* 89314 89413: gap of 100 bp
* 89414 98132: contig of 8719 bp in length
* 98133 98232: gap of 100 bp
* 98233 107469: contig of 9237 bp in length

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* 107470 107569: gap of 100 bp
* 107570 117873: contig of 10304 bp in length
* 117874 117973: gap of 100 bp
* 117974 130973: contig of 13000 bp in length
* 130974 131073: gap of 100 bp
* 131074 143236: contig of 12163 bp in length
* 143237 143336: gap of 100 bp
* 143337 154478: contig of 11142 bp in length
* 154479 154578: gap of 100 bp
* 154579 169967: contig of 15389 bp in length
* 169968 170067: gap of 100 bp
* 170068 187347: contig of 17280 bp in length
* 187348 187447: gap of 100 bp
* 187448 205736: contig of 18289 bp in length.

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Matches 114; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

QY 223 aggaatgtgctcgctcgatgggaggatgcacagctgtgtgacgtgcgcgctgcacaggt 282
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 154301 AGGAGAGTGTATGAGAGGGTGGAGATGCTACTGTGCACACTGTCTCTCTCAGGT 154360

QY 283 tcaaggaggactgggcttcgaagaatgcagccctgtgtgactgcgcagctgtgtgaacc 342
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 154361 AACACAGCAGCTGGGGCCACCACACATGTCAGAGATGCATCCTGTGTCATCAATC 154420

QY 343 gcttcagaagcaaatgttcagccaccagtcagtcacatctgcgggactcgttcgacc 402
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Db 154421 GCGTTCAAGGTGAAGTCGCGACATACCTCTAAATGCTGTGTGTGGGACTGTGTGCCNN 154480

QY 403 gatttataggagcgaactctgcgcttcacagacatggagtgtgtgccttggag 462

Db 154481 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 154540

QY 463 accctctctcttcacgaaccgactgtgccagcaggtcaacctgtgaagat 517
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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RESULT 14
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DEFINITION      Homo sapiens chromosome 3 clone RP11-767C1 map 3p, WORKING DRAFT
AC034198
VERSION          AC034198.4
KEYWORDS         HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE           human.
ORGANISM         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 160214)
Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H.,
Dong,W., Fan,H., Feng,X., Guan,Q., Gu,X., Guo,D., He,L., Hu,S.,
Huang,F., Jin,Y., Kang,N., Li,C., Li,G., Li,J., Li,L.,
Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W., Li,Y.,
Luo,J., Niu,Y., Qi,Q., Qi,X., Song,S., Sun,M., Sun,W., Sun,X.,
Tao,R., Wang,H., Wang,J., Wang,L., Wang,L., Wang,L., Wang,R.,
Wang,X., Wang,X., Wang,Y., Wu,D., Wu,Q., Xie,F., Xuan,Z., Xue,Y.,
Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G., Zhang,H., Zhang,H.,
Zhang,L., Zhang,M., Zhang,X., Zhang,X., Zhang,Y., Zhang,Y.,
Zhang,Z., Zhu,B., Yu,J. and Yang,H.
Chromosome 3p genomic sequence
Unpublished
2 (bases 1 to 160214)
Kang,N., Hu,S., Dong,W., Wang,J., Zhang,Y., Zhang,H., Liu,B.,
Bao,W., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y., Niu,Y.,
Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H., Liu,Y.,
Li,G., Li,C., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L., Guo,D.,
Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L., Feng,X., Yu,J.
and Yang,H.
Direct Submission
Submitted (05-APR-2000) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
On Sep 19, 2000 this sequence version replaced gi:8101278.
-----Genome Center
Center:Beijing Center
Center code:Beijing
Website:http://hgctgtp.ac.cn
http://www.genomics.org.cn
Contact:hgctgtp.ac.cn
----- Project Information

Center project name:il% project
Center clone name: RP11-767C1
----- Summary Statistics
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator; ET 5% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 155354 bases at least Q40
Consensus quality: 160750 bases at least Q30
Consensus quality: 164545 bases at least Q20
Insert size: 150147; sum-of-contigs
Quality coverage: 4.62x in Q20 bases;sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 25 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1071: contig of 1071 bp in length
* 1171: gap of unknown length
* 1172: contig of 1083 bp in length
* 2255: gap of unknown length
* 2355: contig of 1497 bp in length
* 3852: gap of unknown length
* 3952: contig of 1344 bp in length
* 5295: gap of unknown length
* 5395: contig of 1070 bp in length
* 5396: gap of unknown length
* 6465: gap of unknown length
* 6565: contig of 1292 bp in length
* 6566: gap of unknown length
* 7858: gap of unknown length
* 7957: contig of 1237 bp in length
* 9195: gap of unknown length
* 9294: contig of 1744 bp in length
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* 11038: contig of 3282 bp in length
* 11139: gap of unknown length
* 14421: contig of 3344 bp in length
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* 17865: contig of 3306 bp in length
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* 21271: contig of 3680 bp in length
* 21371: gap of unknown length
* 25051: contig of 5474 bp in length
* 25151: gap of unknown length
* 30625: contig of 7047 bp in length
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* 37771: contig of 4276 bp in length
* 37871: gap of unknown length
* 42147: contig of 7505 bp in length
* 42148: gap of unknown length
* 42247: contig of 7441 bp in length
* 42248: gap of unknown length
* 49753: contig of 6233 bp in length
* 49853: gap of unknown length
* 57294: contig of 8794 bp in length
* 57394: gap of unknown length
* 63627: contig of 10918 bp in length
* 63726: gap of unknown length
* 63727: contig of 11575 bp in length
* 72521: gap of unknown length
* 72621: contig of 12308 bp in length
* 83538: gap of unknown length
* 83539: contig of 12790 bp in length
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* 95214: contig of 17829 bp in length
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* 95314: contig of 21674 bp in length
* 107621: gap of unknown length
* 107622: contig of 12790 bp in length
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* 120512: contig of 17829 bp in length
* 120612: gap of unknown length
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* /organism="Homo sapiens"

FEATURES
source
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* 132824 180511: contig of 47688 bp in length.

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FEATURES
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/chromosome="3p"
/clone="Rp11-588p9"

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Best Local Similarity	48.43;	Pred. No. 0.91;		
Matches 121;	Conservative 0;	Mismatches 129;	Indels 0;	Gaps 0;
QY 681	tacaacgctctgagctgtcgtgtcttgacagacctcagctccacgaatatgccacaga	740		
Db 114940	TCCAAACTCTCTGTGCGCGGGGGCAATTCCCTTCCCTGTTGCAGCAGATTCCACCCC	114999		
QY 741	gcctgtctgccagtcgcccgctgactcagtcagacctgcggccggtgcgcttgcctccca	800		
Db 115000	GCCCTGCCCCCACTGCCCGCCCCACGGGAAAGTGCCCGGGAGTGAGCGGTGGACAGGCA	115059		
QY 801	tccatgtgtcgtgagggagcctgcagcccaacccgcgcactcttgtgtggtgggtgcac	860		
Db 115060	TCCCGGTGTCTCAGTTCAGGTGTCTGGGCCAGCTCGGACACACGCGCCGGAGGGCAG	115119		
QY 861	tctcagccagctcttcaggaagaacagcagccagccagccggggagatggtgccacattc	920		
Db 115120	ACAGGGCAGCGAGACAGCCCAAGGCTCCAGACAGCCGCTGACAGGCTGTCCAGCTGC	115179		
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Db 115180	ATCGGGTCTC	115189		

Search completed: March 2, 2001, 12:59:17
Job time: 32956 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 12:41:53 ; Search time 553.05 Seconds
(without alignments)
1157.453 Million cell updates/sec

Title: US-09-380-276A-2

Perfect score: 1704

Sequence: 1 gggaaactgagaactccaa.....gaccagagtagtacttttc 1704

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 18781343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1702.4	99.9	1704	V33361	Nucleotide sequenc
2	1690	99.2	2185	20 X24978	Human TRAIN-R cDNA
3	1290.4	75.7	1496	19 V33362	Nucleotide sequenc
4	1288.8	75.6	1502	20 X08689	Novel nucleotide s
5	1270	74.5	1489	20 X23415	Human hAPO4-alpha
6	835.6	49.0	987	20 X59346	Human NTR-5 cDNA.
7	823	48.3	1678	20 X23413	Mouse MAP04-alpha
8	460.8	27.0	886	20 X23414	Mouse MAP04-alpha
9	460.8	27.0	942	20 X24977	Mouse TRAIN-R (lon
10	460.8	27.0	981	20 X87394	Mouse STRIFE1 (ran
11	447.2	26.2	893	20 X84622	Human TNFR superfa
12	362.6	21.3	538	20 X59345	Mouse NTR-5 cDNA.

13	361.6	21.2	371	19	V11422	Human secreted pro
14	326.6	19.2	591	20	X23417	Mouse MAP04-gamma
15	326.6	19.2	599	20	X24976	Mouse TRAIN-R (sho
16	326.6	19.2	623	20	X84623	Mouse TNFR superfa
17	326.6	19.2	636	21	X92408	cDNA encoding murf
18	326.6	19.2	655	20	X87395	Mouse STRIFE2 (tan
19	208.2	12.2	1133	20	X23416	Rat RAP04-alpha DN
20	154.8	9.1	932	21	X29411	cDNA encoding huma
21	90.4	5.3	791	20	X24979	Clone G156 encodi
22	88.6	5.2	396	20	X23418	Mouse MAP04-beta D
23	87.4	5.1	181	19	V11423	Human secreted pro
24	87.4	5.1	201	20	X86655	EST clone AX92. H
25	81.2	4.8	546	21	X29410	cDNA encoding huma
26	77.8	4.6	474	21	X29409	cDNA encoding huma
27	44	2.6	10732	21	A10594	Gene encoding a su
28	37.4	2.2	1290	20	X23121	Human TANGO 129 (T
29	37.4	2.2	2570	20	X23120	Human TANGO 129 (T
30	37.4	2.2	2703	21	D00061	Human tumour necro
31	36.8	2.2	326	11	Q05546	Fragment 41-3 of t
32	36.4	2.1	1602	15	Q72217	Human adrenergic r
33	36.4	2.1	1978	15	Q72212	Truncated human al
34	36.4	2.1	1987	16	T11624	Human truncated al
35	36.4	2.1	1997	16	T11600	Human alpha-1C adr
36	36.4	2.1	1998	15	Q72213	Human alpha-1C adr
37	36.4	2.1	2004	16	T11599	Human alpha-1C adr
38	36.4	2.1	2005	15	Q72211	Human alpha-1C adr
39	36.2	2.1	330	21	A15982	Human protein clon
40	36.2	2.1	659	21	A15992	Human protein clon
41	36.2	2.1	2486	17	T09866	Human neurotransmi
42	36	2.1	2067	20	V99092	DNA methyltransfer
43	36	2.1	19440	20	V99129	DNA methyltransfer
44	35.6	2.1	1150	20	Z06928	Streptomyces hygro
45	35.2	2.1	1050	21	Z58975	Human cytoskeletal

ALIGNMENTS

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DT 02-DEC-1998 (first entry)
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DE Nucleotide sequence of human alpha-OAF065.
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KW Human; alpha-OAF065; stroma cell; antibody; inflammatory;
KW cytokine-mediated disease; rheumatism; ulcerative colitis; ss.
XX
OS Homo sapiens.
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FH Key Location/Qualifiers
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FT sig_peptide 45..119
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FT mat_peptide 120..1295
FT /tag= c
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WO9838304-Al.
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03-SEP-1998.
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26-FEB-1998; 98WO-JP00799.
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27-FEB-1997; 97JP-0043143.
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PA (ONOY ) ONO PHARM CO LTD.
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[illegible]

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QY 1687 ccagagatatacttttc 1704
Db 1821 ccagagatatacttttc 1838

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DT 02-DEC-1998 (first entry)
XX Nucleotide sequence of human beta-OAF065.
DE Human; beta-OAF065; stroma cell; antibody; inflammatory;
KW cytokine-mediated disease; rheumatism; ulcerative colitis; ss.
XX Homo sapiens.
XX
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FT CDS 45..1316
FT FT /*tag= a
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FT sig_peptide 45..119
FT FT /*tag= b
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FT FT /*tag= c
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FT FT /transl_except= (pos:714..716, aa= Arg)
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PN W09838304-A1.
XX
PD 03-SEP-1998.
XX
PF 26-FEB-1998; 98WO-JP00799.
XX
PR 27-FEB-1997; 97JP-0043143.

XX (ONOY) ONO PHARM CO LTD.
XX Fukushima D, Konishi M, Tada H;
XX WPI; 1998-481205/41.
DR P-PSDB; W70387.
XX Membrane polypeptide expressed by human stroma cells, and antibodies
PT recognising it - for treatment of inflammatory and other
PT cytokine-mediated diseases.
XX Disclosure; Pages 40-41; 54pp; Japanese.
XX This is the nucleotide sequence of the human beta-OAF065, used in
CC the method of the invention. The process involves the use of peptides
CC expressed by stroma cells, and its antibodies are used for in the
CC prevention and treatment of inflammatory and other cytokine-mediated
CC diseases such as rheumatism, ulcerative colitis.
XX Sequence 1496 BP; 388 A; 360 C; 372 G; 376 T; 0 other;
SQ
Query Match 75.7%; Score 1290.4; DB 19; Length 1496;
Best Local Similarity 99.9%; Pred. NO. 0;
Matches 1291; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 gggaacgtgagaactctcccaacaataatacatattgataagaagaatggcttttaaaagtgc 60
Db 1 gggaacgtgagaactctcccaacaataatacatattgataagaagaatggcttttaaaagtgc 60
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QY 421 aactgtcggctttcaagacatggagtgtgcttgtgagaccctctccctccctacg 480
Db 421 aactgtcggctttcaagacatggagtgtgcttgtgagaccctctccctccctacg 480
QY 481 aaccgcaactgtgcagcaaggttcaactcgtgaagatgcgctccagggcctccagcccac 540
Db 481 aaccgcaactgtgcagcaaggttcaactcgtgaagatgcgctccagggcctccagcccac 540
QY 541 gggacacgctggtgctgctgttatctgcagcgtcttgcgcccgcctctgctgcccctgc 600
Db 541 gggacacgctggtgctgctgttatctgcagcgtcttgcgcccgcctctgctgcccctgc 600
QY 601 tcatcctctgtgtcatctattgttaagagacagtttatggagaagaacccagctggtctc 660
Db 601 tcatcctctgtgtcatctattgttaagagacagtttatggagaagaacccagctggtctc 660
QY 661 tgcgggtcaacagagacattcagtaacaacggctctgagctgtctgtcttgacagacctcagc 720
Db 661 tgcgggtcaacagagacattcagtaacaacggctctgagctgtctgtcttgacagacctcagc 720

Db	661	tgcggtcagcagagacattcagtaacaaggctctgagctgtctgtctgacagacctcagc	720
Qy	721	tccacgaatatgccacagagcctgtccagtgccgcgtgtaactcagtgacacattgcg	780
Db	721	tccacgaatatgccacagagcctgtccagtgccgcgtgtaactcagtgacacattgcg	780
Qy	781	ggcggctgcgcttgcctccatccatctgtctgtgaggagcctgcagcccacaaccgcga	840
Db	781	ggcggctgcgcttgcctccatccatctgtctgtgaggagcctgcagcccacaaccgcga	840
Qy	841	ctcttggttggtgggtgcattctgcagccagctcttcaggccaagaaacgcagccagccg	900
Db	841	ctcttggttggtgggtgcattctgcagccagctcttcaggccaagaaacgcagccagccg	900
Qy	901	gggagatggtgcggaactttcttcggatccctccagccagctccatctgtggcgagttttcag	960
Db	901	gggagatggtgcggaactttcttcggatccctccagccagctccatctgtggcgagttttcag	960
Qy	961	atgcctggcctctgtgcagaatcccatgggtgtggaacaacatctctttttgtgactctt	1020
Db	961	atgcctggcctctgtgcagaatcccatgggtgtggaacaacatctctttttgtgactctt	1020
Qy	1021	atcctgaactcactggagaagacattcattctctcattccagaaacttgaaagctcaacgt	1080
Db	1021	atcctgaactcactggagaagacattcattctctcattccagaaacttgaaagctcaacgt	1080
Qy	1081	ctttgattcacaatagcagctcaagatttggttggtgggcgtgtccagctccagctcatt	1140
Db	1081	ctttgattcacaatagcagctcaagatttggttggtgggcgtgtccagctccagctcatt	1140
Qy	1141	ctgaaactttacagcagctactgatttatctagatatacaaacacacactggtagaatcag	1200
Db	1141	ctgaaactttacagcagctactgatttatctagatatacaaacacacactggtagaatcag	1200
Qy	1201	catcaactcaggatgcactaacatagaaagccagctagatcagagagatggcgctatca	1260
Db	1201	catcaactcaggatgcactaacatagaaagccagctagatcagagagatggcgctatca	1260
Qy	1261	tccaccagccactcagacgtccctccaggaa	1292
Db	1261	tccaccagccactcagacgtccctccaggta	1292
RESULT 4			
X08689	ID	X08689 standard; cDNA; 1502 BP.	
XX	AC	X08689;	
XX	DT	27-SEP-1999 (first entry)	
XX	DE	Novel nucleotide sequence encoding new protein (Clone AX92_3).	
XX	KW	Polynucleotide; protein; nutrition; cytokine; cell proliferation;	
XX	KW	cell differentiation; immunostimulation; immunosuppression;	
XX	KW	hematopoiesis regulation; tissue growth; activin; inhibin;	
XX	KW	chemotaxis; chemokinesis; haemostasis; thrombolysis; receptor;	
XX	KW	ligand; anti-inflammatory; tumour suppression; gene therapy; ds.	
OS	XX	Homo sapiens.	
XX	XX	Location/Qualifiers	
FH	Key	51..1322	
FT	CDS	/tag= a	
FT	FT	/product= "Novel protein"	
XX	XX	WO9920644-A1.	
XX	XX	29-APR-1999.	
XX	XX	16-OCT-1998; 98WO-US22034.	
XX	XX	18-OCT-1997; 97US-0955557.	

(GEMY) GENETICS INST INC.

Agostino MJ, Bowman MR, Evans C, Jacobs K, Lavallie ER,
McCoy JM, Merberg D, Racie LA, Spaulding V, Treacy M;

WPI: 1999-288272/24.

P-PSDB: W85724.

New polynucleotides encoding secreted human proteins

Claim 32; Page 116; 136pp; English.

The new human secreted proteins are encoded by polynucleotides obtained from human placenta, adult testes, fetal kidney, fetal brain, adult brain, adult brain and adult blood cDNA libraries. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotides are also stated to be useful for gene therapy. The sequences are identified by a secretory leader sequence motif in the polynucleotide and it is thought that the encoded proteins have biological activity by virtue of their secreted nature. This clone was designated AX92_3. A probe for this clone is described in X08704.

Sequence 1502 BP; 388 A; 362 C; 375 G; 377 T; 0 other;

Query Match 75.6%; Score 1288.8; DB 20; Length 1502;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1290; Conservative 0; Mismatches 2; Indels 0; Gaps

Qy 1 ggggaactgagaactctccaacaataatacatattgataagaagatggtttaaagatgc 60
Db 7 ggggaactgagaactctccaacaataatacatattgataagaagaaggctttaaagatgc 66
Qy 61 tactagaacaagaaacggttttcaactcttttagtattactaggctattgtcatgta 120
Db 67 tactagaacaagaaacggttttcaactcttttagtattactaggctattgtcatgta 126
Qy 121 aagtgaacttgtaaacaggagactgtagacagacaagaattcagggtatcggtctggaact 180
Db 127 aagtgaacttgtaaacaggagactgtagacagacaagaattcagggtatcggtctggaact 186
Qy 181 gtgttcctctgaaccagtggtggccaggagcatgagttgtctaaaggaatgtggcttcggct 240
Db 187 gtgttcctctgaaccagtggtggccaggagcatgagttgtctaaaggaatgtggcttcggct 246
Qy 241 atggggaggatgcacagtgtgtgacgtgcgcggctgcacaggttcaaggaggactggggct 300
Db 247 atggggaggatgcacagtgtgtgacgtgcgcggctgcacaggttcaaggaggactggggct 306
Qy 301 tccagaataccaagccctgtctgagactgcagctggtgaaccgcttccagaaggcaaat 360
Db 307 tccagaataccaagccctgtctgagactgcagctggtgaaccgcttccagaaggcaaat 366
Qy 361 gttcagccaccagtgatgccatctgcgggagctgcttgcaggatattatagaagacga 420
Db 367 gttcagccaccagtgatgccatctgcgggagctgcttgcaggatattatagaagacga 426
Qy 421 aactgtgcgctttcagaacaatggagtggtgtgctgtgagagacctctctctctacg 480
Db 427 aactgtgcgctttcagaacaatggagtggtgtgctgtgagagacctctctctctacg 486
Qy 481 aaccgcactgtgccagcaagaagtcgaacctgtgaagatcgctgtccagggctccagcccac 540

Query Match	75.6%	Score 1288.8;	DB 20;	Length 1502;		
Best Local Similarity	99.8%;	Pred. No. 0;				
Matches 1290;	Conservative	0;	Mismatches	2; Indels	0; Gaps	0;
Qy	1	gggaacgtagaaactccaacaataatcacatttgataagaagaatggtctttaaagtgc	60			
Dbb	7	gggaacgtagaaactccaacaataatcacatttgataagaagaatggtctttaaagtgc	66			
Qy	61	tactagaacaagaaaaaacgtttttcactcttttagtattactaggctatttgtcaqtga	120			
Dbb	67	tactagaacaagaaaaaacgtttttcactcttttagtattactaggctatttgtcaqtga	126			
Qy	121	aagtgaacttggaaaacaggagactgtagacagcaagaattcaggagatcggtctggaaact	180			
Dbb	127	aagi-gacttggaaaacaggagactgtagacagcaagaattcaggagatcggtctggaaact	186			
Qy	181	gtgttcctcgtcaaacacagtgtgggcaggacatggagttgtcttaagaaatgtggcttcggct	240			
Dbb	187	gtgttcctcgtcaaacacagtgtgggcaggacatggagttgtcttaagaaatgtggcttcggct	246			
Qy	241	atggggagagatgcacagtgtgtgacgtgccgcgtgcacaggttcaaaggagacctggggct	300			
Dbb	247	atggggagagatgcacagtgtgtgacgtgccgcgtgcacaggttcaaaggagacctggggct	306			
Qy	301	tccgaaatgcgaaccctgtctgactgcgcagctgggtgaacgcgttttcagaagagcaaat	360			
Dbb	307	tccgaaatgcgaaccctgtctgactgcgcagctgggtgaacgcgttttcagaagagcaaat	366			
Qy	361	gttcagcccacagtgatgcattctgcggggagctgcttgcaggatatttatagggaagcga	420			
Dbb	367	gttcagcccacagtgatgcattctgcggggagctgcttgcaggatatttatagggaagcga	426			
Qy	421	aacttgtcgggtttcaagacatggaagtgtgtgcttgtggagacccctcctcttaccg	480			
Dbb	427	aacttgtcgggtttcaagacatggaagtgtgtgcttgtggagacccctcctcttaccg	486			
Ov	481	aaccgcactgtggccagcaaggtcaacctctggaagatcgcgtccagggccttccagggccac	540			

|||||
Db 487 aaccgcactgtgcagcaaggtcaacctcgtgaagtgcggtccacggtccctccagccac 546
Qy 541 ggacacggcgctggctgcgtttatctgcagcgtctctggccacggtccctctgctgcctgc 600
Db 547 gggacacggcgctggctgcgtttatctgcagcgtctctggccacggtccctctgctgcctgc 606
Qy 601 tcatctctgtgcattctctgttaagagacagtttatggagagaaacccagctggtctc 660
Db 607 tcatctctgtgcattctctgttaagagacagtttatggagagaaacccagctggtctc 666
Qy 661 tgcgggtacagagacattcagtaacacggctctgcagctctgcgtgtctgttcagacacctcagc 720
Db 667 tgcgggtacagagacattcagtaacacggctctgcagctctgcgtgtctgttcagacacctcagc 726
Qy 721 tccacgaatatgccacagagcgtctgcagctgcgcgcgcgctgactcagtgacagacctgcg 780
Db 727 tccacgaatatgccacagagcgtctgcagctgcgcgcgcgctgactcagtgacagacctgcg 786
Qy 781 ggcgggtgcgctgtctcccatccatgtgctgtgagagggcctgcagccccaacccggcga 840
Db 787 ggcgggtgcgctgtctcccatccatgtgctgtgagagggcctgcagccccaacccggcga 846
Qy 841 ctcttggtgtgggtgctcattctgcagccagctcttcaggcaagaaacgagggccagcgg 900
Db 847 ctcttggtgtgggtgctcattctgcagccagctcttcaggcaagaaacgagggccagcgg 906
Qy 901 ggagatggtgcgacgtttcttcggatccctcagcagctccatctctgtgcggagttttcag 960
Db 907 ggagatggtgcgacgtttcttcggatccctcagcagctccatctctgtgcggagttttcag 966
Qy 961 atgcctggcctctgatgcagaatcccatgggtggtgacacatctctttttgtgactctt 1020
Db 967 atgcctggcctctgatgcagaatcccatgggtggtgacacatctctttttgtgactctt 1026
Qy 1021 atcctgaactcactgagagacattcattctctcaatccagaaacttgaaagctcaact 1080
Db 1027 atcctgaactcactgagagacattcattctctcaatccagaaacttgaaagctcaact 1086
Qy 1081 ctttgattcaaatagacagtcagattgtgtgtggtggtggtggtggtggtggtggtggtggt 1140
Db 1087 ctttgattcaaatagacagtcagattgtgtgtggtggtggtggtggtggtggtggtggtggt 1146
Qy 1141 ctgaaacactttacagcagctactgatttactagatataacacacactggttagaatcag 1200
Db 1147 ctgaaacactttacagcagctactgatttactagatataacacacactggttagaatcag 1206
Qy 1201 catcaactcaggtgactaactatgagaagccagctagatccaggaggtggcgctatca 1260
Db 1207 catcaactcaggtgactaactatgagaagccagctagatccaggaggtggcgctatca 1266
Qy 1261 tccaccagccactcagcgtccctccaggaa 1292
Db 1267 tccaccagccactcagcgtccctccaggaa 1298

RESULT 5
X23415
ID X23415 standard; DNA; 1489 BP.
XX AC X23415;
XX DT 18-JUN-1999 (first entry)
XX DE Human hAPO4-alpha DNA.
XX KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW developmental abnormality; gestational abnormality; prostate cancer;
KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW apoptosis; human; APO4-alpha; ss.
XX OS Homo sapiens.

XX Key Location/Qualifiers
FH CDS 65..1336
FT /*tag= a
FT /product= "hAPO4-alpha"
XX
PN W09911791-A2.
XX
PD 11-MAR-1999.
XX
PF 04-SEP-1998; 98WO-US18393.
XX
PR 05-SEP-1997; 97US-0924634.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Chaudhary PM;
XX
DR WPI; 1999-205191/17.
DR P-PSDB; W93581.
XX
PT New Tumor Necrosis Factor family receptor polypeptides and ligands -
PT useful for diagnosis and treatment of prostate cancer and
PT developmental or gestational abnormalities
XX
PS Example IV; Fig 7C; 156pp; English.
XX
CC This invention describes isolated Tumor Necrosis Factor (TNF) family
CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC their active fragments. APO4 is useful for diagnosing prostate cancer
CC by determining levels of APO4 in an individual. prostate cancer can also
CC be treated using APO4 selective binding agents linked to a therapeutic
CC moiety. APO4 polypeptides are also useful for identifying selective
CC binding agents, useful in diagnosis/treatment of disease by binding of
CC agents to the polypeptide/active fragment which is extracellular, or
CC expressed on the cell surface. The binding is preferably performed in
CC vivo. APO4 polypeptides/ active fragments are also useful for screening
CC for agonists and antagonists by binding and observing the changer in APO4
CC activity. Effective pharmacological agents useful in diagnosis or
CC treatment of disease are also identified using APO4 polypeptides/active
CC fragments and APO4 signal transducer molecules that specifically interact
CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC activity. The method is performed in vivo or in vitro. APO polypeptides
CC are all useful as immunogens for preparing antibodies. APO4 is also
CC useful for diagnosis/treatment of developmental or gestational
CC abnormalities. APO8 was transfected to human breast carcinoma cell line
CC MCF-7, and induced apoptosis.
XX
SQ Sequence 1489 BP; 361 A; 366 C; 380 G; 382 T; 0 other;

Query Match 74.5%; Score 1270; DB 20; Length 1489;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1276; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 7 gtagaactctccaacataacatttataagaagaagatggctttataaagtctactag 66
Db 27 gaagaactctccaacataacatttataagaagaagatggctttataaagtctactag 86
Qy 67 aacaagagaaaacgtttttcacctcttttagtattactaggtattgtgaaactgtttc 126
Db 87 aacaagagaaaacgtttttcacctcttttagtattactaggtattgtgaaactgtt 146
Qy 127 cttgtgaacacaggagactgtagacacagaattccaggatcgggtctgaaactgtttc 186
Db 147 cttgtgaacacaggagactgtagacacagaattccaggatcgggtctgaaactgtttc 206
Qy 187 cctgcacacagtgctggccagcagctaggttctcagaagatgtgcttcggtatgggg 246
Db 207 cctgcacacagtgctggccagcagctaggttctcagaagatgtgcttcggtatgggg 266
Qy 247 aggatgcacagtgctgacgtgccgctgcacaggttcacaggaggactggggtccaga 306

Db 267 aggatgcagtgctggtgcccgtgcacaggttcaaggagactggggcttccaga 326
Qy 307 aatgcaagccctgtctgactgcagctggtggaacgctttcagaagcaaatgtttcag 366
Db 327 aatgcaagccctgtctgactgcagctggtggaacgctttcagaagcaaatgtttcag 386
Qy 367 ccacagtgatgccatctgcgggactgcttgccaggatatttataggagacgaaacttg 426
Db 387 ccacagtgatgccatctgcgggactgcttgccaggatatttataggagacgaaacttg 446
Qy 427 tcgggtttcaagacatgagtggtgcttcttggaacccctctctctcttctacgaaccgc 486
Db 447 tcgggtttcaagacatgagtggtgcttcttggaacccctctctctcttctacgaaccgc 506
Qy 487 actgtgcagcaaggtcaacctctgagatgcgctccacgctccacgctccacgacgggaca 546
Db 507 actgtgcagcaaggtcaacctctgagatgcgctccacgctccacgctccacgacgggaca 566
Qy 547 cggcgctggctgcgttatctgcagcgtcttgccaccgctcgtgctgcccctgctcatcc 606
Db 567 cggcgctggctgcgttatctgcagcgtcttgccaccgctcgtgctgcccctgctcatcc 626
Qy 607 tctgtcatctattgtgaagacagtttatggagaagaaccccgctggtctctgcggt 666
Db 627 tctgtcatctattgtgaagacagtttatggagaagaaccccgctggtctctgcggt 686
Qy 667 cacaggaattcagtacacagcgtctgagctgctgcttcttgacagacctcagctccacg 726
Db 687 cacaggaattcagtacacagcagctgagctgctgcttcttgacagacctcagctccacg 746
Qy 727 aatagccacagagcctgctgccagtgccgcgctgactcagtcagacctgcgggcgg 786
Db 747 aatagccacagagcctgctgccagtgccgcgctgactcagtcagacctgcgggcgg 806
Qy 787 tgcgttctcccatccatctgctgtgaggaagcctgcagcccaacccggcgactcttg 846
Db 807 tgcgttctcccatccatctgctgtgaggaagcctgcagcccaacccggcgactcttg 866
Qy 847 gttgtggagtgctattctcagccagcttctcaggaagcaaacgacggcccgaggaga 906
Db 867 gttgtggagtgctattctcagccagcttctcaggaagcaaacgacggcccgaggaga 926
Qy 907 tgggtccgactttcttcggatccctcagcagctcctatctgtgagtggtttcagatgct 966
Db 927 tgggtccgactttcttcggatccctcagcagctcctatctgtgagtggtttcagatgct 986
Qy 967 ggcctctgatgcagatcccatgggtggtgacaacatctcttttctgactcttactctg 1026
Db 987 ggcctctgatgcagatcccatgggtggtgacaacatctcttttctgactcttactctg 1046
Qy 1027 aactcactggagaagacattctctcaatccgaacttgaaagctcaacgctcttcttg 1086
Db 1047 aactcactggagaagacattctctcaatccgaacttgaaagctcaacgctcttcttg 1106
Qy 1087 attcaaatagcagtcgaagatttggtggtgggctgttccagtcagctctctctgaaa 1146
Db 1107 attcaaatagcagtcgaagatttggtggtgggctgttccagtcagctctctctgaaa 1166
Qy 1147 actttacagcagctactgatttatctagatataaacacacactggtagaaatcagatcaa 1206
Db 1167 actttacagcagctactgatttatctagatataaacacacactggtagaaatcagatcaa 1226
Qy 1207 ctccagatgactaactatgagaagcagctagatcaggagagtggtgcgtatctccacc 1266
Db 1227 ctccagatgactaactatgagaagcagctagatcaggagagtggtgcgtatctccacc 1286
Qy 1267 cagccactcagacgtccctccaggaa 1292
Db 1287 cagccactcagacgtccctccaggta 1312

RESULT 6

X59346
ID X59346 standard; cDNA; 987 BP.
XX
AC X59346;
XX
DT 20-SEP-1999 (first entry)
XX
DE Human NTR-5 cDNA.
XX
KW NTR-5; human; receptor; signal transduction; bone; muscle;
KW diagnosis; therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT sig_peptide 1..57
FT /*tag= a
FT mat_peptide 58..987
FT /*tag= b
XX
FT WO9933967-A2.
XX
PN 08-JUL-1999.
XX
PD
XX
PF 28-DEC-1998; 98WO-US27688.
XX
PR 29-DEC-1997; 97US-0068925.
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Valenzuela DM;
XX
DR WPI: 1999-419102/35.
DR P-PSDB; Y06400.
XX
PT New mammalian receptor NTR-5 polypeptides
PS Claim 2a; Page 21-22; 27pp; English.
XX
CC This is the claimed coding region of human cDNA encoding a novel
CC receptor, designated NTR-5 (see Y06400), that shows homology to
CC osteoprotegerin and tumour necrosis factor receptor. The cDNA was
CC isolated from a heart cDNA library using mouse NTR-5 cDNA (see
CC X59345) as probe. Homology to osteoprotegerin suggests that NTR-5
CC is involved in the regulation of bone mass, and may be useful for
CC regulating development, proliferation and death of osteoblast or
CC osteoclast cells or for regulating muscle metabolism, and that it
CC may be implicated in muscle diseases or disorders. A host-vector
CC system for production of NTR-5 is claimed. NTR-5 polypeptides can
CC be used as immunogens and in screening assays to identify NTR-5
CC ligands, agonists and antagonists. The NTR-5 polynucleotide is
CC useful as a diagnostic tool, and as a source of probes and primers.
CC The invention also provides for diagnostic and therapeutic methods
CC based on the interaction of NTR-5 and agents that initiate signal
CC transduction through binding to NTR-5.
XX
SQ Sequence 987 BP; 220 A; 251 C; 278 G; 238 T; 0 other;

Query Match 49.0%; Score 835.6; DB 20; Length 987;
Best Local Similarity 99.5%; Pred. No. 3.6e-251;
Matches 838; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 45 atggccttaaaagtctactagaacaagaaaacgcttttctactcttttagtattacta 104
Db 1 atggccttaaaagtctactagaacaagaaaacgcttttctactctttttagtattacta 60
Qy 105 ggctattgttcataaagtactgtgaacacagagactgtagacagacaagaattcagg 164
Db 61 ggctattgttcataaagtactgtgaacacagagactgtagacagacaagaattcagg 120
Qy 165 gatcggctcggaaactgtgttccctgcaccagtgctggccaggatgagtggtctaa 224

Db 121 gacggtgtggaactgtgttccctgcacaccagtggtggccaggcatggaggtgtctaaag 180
QY 225 gaatgtggtctcgctatgaggagatgcacagtgtgtacgtgcgcgctgcacagttc 284
Db 181 gaaatgtggtctcgctatgaggagatgcacagtgtgtacgtgcgcgctgcacagttc 240
QY 285 aaggaggactggggtctccagaaatcgaagccctgtctggaactgcgcagtggtgaaccgc 344
Db 241 aaggaggactggggtctccagaaatcgaagccctgtctggaactgcgcagtggtgaaccgc 300
QY 345 ttccagaaggcaaatgttccagccaccagtgatgccatctgcgggactgcttgccaggga 404
Db 301 ttccagaaggcaaatgttccagccaccagtgatgccatctgcgggactgcttgccaggga 360
QY 405 ttctataggagacgaactgtcgctttcagaagacatgagtggtgcttcttgagac 464
Db 361 ttctataggagacgaactgtcgctttcagaagacatgagtggtgcttcttgagac 420
QY 465 cctcctcctcttaccgaaccgactgtgccagcaagtgcaacctcgtgaagatcgctcc 524
Db 421 cctcctcctcttaccgaaccgactgtgccagcaagtgcaacctcgtgaagatcgctcc 480
QY 525 acggctccagccacgggacacggcgctggtgcggttatctgcagcgctctgcccacc 584
Db 481 acggctccagccacgggacacggcgctggtgcggttatctgcagcgctctgcccacc 540
QY 585 gtccgtggtcctgcctcctcctctgtctcattctattgtaagagacagtttatggagaag 644
Db 541 gtccgtggtcctgcctcctcctctgtctcattctattgtaagagacagtttatggagaag 600
QY 645 aaaccagctggtctctgcggtcacaggacattcagtcacacggctcctgagctgtcgtgt 704
Db 601 aaaccagctggtctctgcggtcgaggacattcagtcacacggctcctgagctgtcgtgt 660
QY 705 ctgtgagacactcagctccacgaatatgccacagagcctgctgcagtgcccctgtgac 764
Db 661 ttgtgagacactcagctccacgaatatgccacagagcctgctgcagtgcccctgtgac 720
QY 765 tcagtgacagctcgggcggtgctgtctcctccatcctgctgtgagagggcctgc 824
Db 721 tcagtgacagctcgggcggtgctgtctcctccatcctgctgtgagagggcctgc 780
QY 825 agccccacccggcgactctgtgtgtggtggtggtcattctgcagccagcttccaggcaaga 884
Db 781 agccccacccggcgactctgtgtgtggtggtggtcattctgcagccagcttccaggcaagg 840
QY 885 aa 886
Db 841 aa 842

RESULT 7
X23413
ID X23413 standard; DNA; 1678 BP.
XX
AC X23413;
XX
DT 18-JUN-1999 (first entry)
XX
DE Mouse mAPO4-alpha (long) DNA.
XX
KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
developmental abnormality; gestational abnormality; prostate cancer;
APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
apoptosis; mouse; mAPO4-alpha; ss.
XX
OS Mus sp.
XX
FH Key
FT CDS 72..1322
FT /*tag= a
FT /product= "mAPO4-alpha"

XX WO9911791-A2.
PN 11-MAR-1999.
XX
PD
XX
PF 04-SEP-1998; 98WO-US18393.
XX
PR 05-SEP-1997; 97US-0924634.
XX
PA (UNIW) UNIV WASHINGTON.
XX
XX Chaudhary PM;
PI
XX WPI; 1999-205191/17.
DR P-PSDB; W93579.
XX
XX New Tumor Necrosis Factor family receptor polypeptides and ligands -
PT useful for diagnosis and treatment of prostate cancer and
PT developmental or gestational abnormalities
XX
XX Example IV; Fig 7A; 156pp; English.
XX
CC This invention describes isolated Tumor Necrosis Factor (TNF) family
receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
CC their active fragments. APO4 is useful for diagnosing prostate cancer
CC by determining levels of APO4 in an individual. Prostate cancer can also
CC be treated using APO4 selective binding agents linked to a therapeutic
CC moiety. APO4 polypeptides are also useful for identifying selective
CC binding agents, useful in diagnosis/treatment of disease by binding of
CC agents to the polypeptide/active fragment which is extracellular, or
CC expressed on the cell surface. The binding is preferably performed in
CC vivo. APO4 polypeptides/ active fragments are also useful for screening
CC for agonists and antagonists by binding and observing the changer in APO4
CC activity. Effective pharmacological agents useful in diagnosis or
CC treatment of disease are also identified using APO4 polypeptides/active
CC fragments and APO4 signal transducer molecules that specifically interact
CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC activity. The method is performed in vivo or in vitro. APO polypeptides
CC are all useful as immunogens for preparing antibodies. APO4 is also
CC useful for diagnosis/treatment of developmental or gestational
CC abnormalities. APO8 was transfected to human breast carcinoma cell line
CC MCF-7, and induced apoptosis.
XX
SQ Sequence 1678 BP; 371 A; 467 C; 466 G; 374 T; 0 other;

Query Match 48.3%; Score 823; DB 20; Length 1678;
Best Local Similarity 71.6%; Pred. NO. 4.5e-247;
Matches 1191; Conservative 0; Mismatches 435; Indels 37; Gaps 7;

QY 22 aataaatacatttgataagaagaatggcttttaaaagtgtactactagacaagaagaaacgt 81
||||| || |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 49 aataaacaagtttggtagagccatggcactcaaggctcctcctcacacagagcgtgc 108
QY 82 ttttctactcttttagtattactaggctattgtcattgaagtgaactgtgtgaaacaggag 141
||||| || |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 109 tcttcgtcgccattctcttctactccacctggcagtgataaagtgtgtcgaaacaggag 168
QY 142 actgtagacagcagaattccagggtcggttctggaactgtgttccctgcacaccagtggtg 201
||||| || |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 169 attgcaggcagcaggattccaagatcgatctggaaactgtgtcctctgcacacagtgcg 228
QY 202 ggcacagcagtgagttgtctaaagaaatggcttcggctatgggagagcagcagtggtg 261
||||| || |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 229 gacctggcagtgagttgtcccaagaaatggcttcggctatgggagagtgatgcacagtggtg 288
QY 262 tgacgtgcgggctgcacaggttccaaggagagctggggtctccagaaatgcacgccctgtc 321
||||| || |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 289 tgccctgcaggccgaccggtttccaagaaagactggggtttccagaagtgtaaagcctgtg 348
QY 322 tggactgcgcagtggtgaaccgctttcagaagagcgaattgttccagccaccagtgatgcca 381
||||| || |||| |||| |||| |||| |||| |||| |||| |||| ||||

Db 349 cggactgtgcgtgtgaaccgctttcagaggcgcaactgtctcacacaccagtgatgctg 408
Qy 382 tctcggggactgctgcagagttttataggaagacaaaactgtgcgctttcaagaca 441
Db 409 tctcggggactgctgcagagttttaccggaagacaaaactgtgtgttttcaagaca 468
Qy 442 tggagtgtgctgtgtgagaccctctctcctctagaaacgacactgtgcagcaagg 501
Db 469 tggagtgtgctgtgcggagaccacctctcctctagaaacacactgtaccagcaagg 528
Qy 502 tcaacctgtgaagatcgctgcacggcctccagcccagggagacgcgctggtgcgcg 561
Db 529 tgaacctgtgaagatcctcctcagctctccagcctcgggacacgctggtgcgcg 588
Qy 562 ttaactgagcgtctggccacgctcctgctgcccctgctcactctctgtgctcatt 621
Db 589 tcaactgagctgtgcggcaggtgtgctgctgcctgctcactctgtgtgctact 648
Qy 622 gtaagagacagtttatgagaagaacccagctgtctctgctgcgttcacagagacattcagt 681
Db 649 gcaagaggcagttcatgagaagaacccagctgtctctgctgcgttcacagagacattcagt 708
Qy 682 acaacgctctgagctgtgctgtgtgttgacagacctcagctccacgaataatgccacagag 741
Db 709 acaatggctctgagctgtcatgtctgtgaccagcctcggctcggcactgtgcccataag 768
Qy 742 cctgctgcagtcgcccgcgtgactcagtgacagacctgcggccgctgctgctcccat 801
Db 769 catgctgacgtatcacgggactcagcccacatgtatgggctgttcaactgtatccgt 828
Qy 802 catgctgtgtgagagcctgcagcccacacccgacactctgtgtgtgggtgcatt 861
Db 829 cctgtgctgtgaagaggccgcagctctgtcccagctgtgctgtggtgtgggtgcgtt 888
Qy 862 ctgcagcagtttccaggcaagaacagcagccgcccggggagatggtgcgcgactttct 921
Db 889 cctccactaccctccagagagaacccggctctgtgggaaacacgatgccagcctct 948
Qy 922 tcggatccctcagcagtcctctgtggcagttttcagatccctgacctgtgatgcaga 981
Db 949 tgggtctgttcccgcttccactcgcggaggtttttctgtatgcttgccttgcctgtgatgcaga 1008
Qy 982 atccatgggtgtgacaacatctctttttgtgactcttctgaactcactggagag 1041
Db 1009 atcctctgggggtg---acagctctctgtgactcttctgaactcactggagag 1065
Qy 1042 acattcattctcactcagaaactgaagctcaagctccttggattcgaataatagcagtc 1101
Db 1066 ataccaattcctcctcaatccgaaacgaaagcacagcactctctgattccagtgcgcc 1125
Qy 1102 aagatttgggtgggtgttccagttccagtcctcactctgaactttacagcagcta 1161
Db 1126 aggatctgggtggagcagctgctctagatcttcttgggaattttcagaactactgact 1185
Qy 1162 ctgatttactagatataacacacactggtgaatcagcatcactcaggatgcactaa 1221
Db 1186 cacctagacatggtgacactggtacagctggtgagcagcgtagtctcaggtgtcctaaa 1245
Qy 1222 cctagagaagcagctagatcagagagtgcgctatcatccaccagccactcagagct 1281
Db 1246 ggaactcagaagagggtggtggaagacagggaaacccgtaactgtagcctgcccacag 1305
Qy 1282 cctccaggaagcttaagaacactgcttcttctcagtagaagcgtgtgctggaaccca 1341
Db 1306 ccttcagagatcctgaag---gccactctcagctgaggtgtggtgtctggaac- 1360
Qy 1342 aagagtactccttctgttagctttagctgagcagctgtggacccttgcactgtcttgg 1401
Db 1361 -----gctgtgtagggcctacagactgagcagctgtt-----gtgctcggaa 1404
Qy 1402 gcaaaaaataactgaacaaactgacggcatttgaagcctttcagcaggtgtcctctga 1461
Db 1405 gcaaaaaataactgaacaaactgacaaacttccatctcttcagcactgactgactga 1464

Qy 1462 gccagaccagctgaagctgaacctcaatgaataacaagaaaaagactcca----ggccg 1517
Db 1465 gccagaccagctgaagctgaacctcaatgaataacaagaaaaagactgactgtagcgcg 1524
Qy 1518 actcatgatactctgactctctctctacatgagaagcttctctgccacaaaagtacttca 1577
Db 1525 gctctgggacatgtcttctctccctaaagcgaacaccttagctggggcca-----atttga 1579
Qy 1578 aagacggatgggtgagctggcagcctatgagattgtggacataatacaagaaacagaaa 1637
Db 1580 aggacccatgggtgaatgtgctgctgtaactgtggaactgtgggcacagca----ggacccagc 1635
Qy 1638 tgccctcatgcttcttctcatgtgtgattgtgttttacaagac 1680
Db 1636 ctggctccttcttctgctccagcgtgaatgtgtgtttcacaagac 1678

RESULT 8
X23414
ID X23414 standard; DNA; 886 BP.
XX
AC X23414;
XX
DT 18-JUN-1999 (first entry)
XX
DE Mouse mAPO4-alpha (short) DNA.
XX
KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
developmental abnormality; gestational abnormality; prostate cancer;
APO6; APO8; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
apoptosis; mouse; mAPO4-alpha; ss.
OS Mus sp.
XX
FH Key Location/Qualifiers
CDS 72..716
FT /*tag= a
FT /product= "mAPO4-alpha short"
XX
PN W09911791-A2.
XX
PD 11-MAR-1999.
XX
PF 04-SEP-1998; 98WO-US18393.
XX
PR 05-SEP-1997; 97US-0924634.
XX
PA (UNIW) UNIV WASHINGTON.
XX
PI Chaudhary PM;
XX
DR WPI; 1999-205191/17.
DR P-PSDB; W93580.
XX
PT New Tumor Necrosis Factor family receptor polypeptides and ligands -
developmental or gestational abnormalities
XX
PS Example IV; Fig 7B; 156pp; English.
XX
CC This invention describes isolated Tumor Necrosis Factor (TNF) family
receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
their active fragments. APO4 is useful for diagnosing prostate cancer
by determining levels of APO4 in an individual. Prostate cancer can also
be treated using APO4 selective binding agents linked to a therapeutic
moiety. APO4 polypeptides are also useful for identifying selective
binding agents, useful in diagnosis/treatment of disease by binding of
agents to the polypeptide/active fragment which is extracellular, or
expressed on the cell surface. The binding is preferably performed in
vivo. APO4 polypeptides/ active fragments are also useful for screening

CC for agonists and antagonists by binding and observing the changer in APO4
CC activity. Effective pharmacological agents useful in diagnosis or
CC treatment of disease are also identified using APO4 polypeptides/active
CC fragments and APO4 signal transducer molecules that specifically interact
CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
CC activity. The method is performed in vivo or in vitro. APO polypeptides
CC are all useful as immunogens for preparing antibodies. APO4 is also
CC useful for diagnosis/treatment of developmental or gestational
CC abnormalities. APO8 was transfected to human breast carcinoma cell line
CC MCF-7, and induced apoptosis.

XX SQ Sequence 886 BP; 204 A; 245 C; 247 G; 190 T; 0 other;

Query Match 27.0%; Score 460.8; DB 20; Length 886;
Best Local Similarity 81.9%; Pred. No. 6.4e-134; Indels 0; Gaps 0;
Matches 531; Conservative 0; Mismatches 117;
QY 22 aataatacatttgataagaagaatggcttttaaaagtgtactagaacaagagaaacgt 81
DB 49 aataaacacgtttggtgagagccatggcactcaaggtctctacctacacagagcgtgc 108
QY 82 ttttcaactcttagtattactaggctatttgcataagtgacttgcgaacaggag 141
DB 109 tcttcgctgcattctctctactccaccctggcgtgaaagtgaagtgcgaacaggag 168
QY 142 actgtagacagcaagaattcaggatcggtctggaactgttccctgcacacagtg 201
DB 169 attgcagggcagcgggaattcaaggatcgatctggaaactgtctctctgcacacagtcg 228
QY 202 ggcagcagtgagtgctcaagaatgtgcttcggtatggggagatgcacagtg 261
DB 229 gactggtcagtgagtgctcaagaatgtgcttcggtatggggagatgcacagtg 288
QY 262 tgcgtgcggcgtgcacaggttcaaggagactggggcttccagaaatgcacacccctgc 321
DB 289 tgccctgcagggcgcacgggttcaaggagactgggggttccagaaagtgaagccatgtg 348
QY 322 tgcactgcagtggtgaaacgctttcagaaggcgaattgttcagccacagtgatgcca 381
DB 349 cggactgtgcgtggtgaaacgctttcagaaggcggccactgtcacacacagtgatgctg 408
QY 382 tctgcggggactgctgcccaggattttataggagacgaactgtgctgctttcaagaca 441
DB 409 tctgcggggactgctgcccaggattttaccgcgaagacaaactggtggttttcaagaca 468
QY 442 tggagtgtgctgttgagacccctctctcttaccgaacgcgactgtgccagcaagg 501
DB 469 tggagtgtgctgtgagacccctctctcttaccgaacgcgactgtaccagcaagg 528
QY 502 tcaacctgtgaagatcgctccacggcctccagccacgggacacggcgtggtgccc 561
DB 529 tgaacctgtggaagatctctccacggctccagccctcgggacacggcgtggtgccc 588
QY 562 ttatctgcagcgtctggtccacggctctggtgcccctgctcctctctgtgtatctatt 621
DB 589 tcactgcagtgtctggtccacggctgtgctgcccctgctcctctgtgtgtatctact 648
QY 622 gtaagagacagtttatggaagaagaacccacagctggctctctgctggttaac 669
DB 649 gcaagaggcagttcatggaagaagaacccacagctgtaagctccccatccc 696

RESULT 9

X24977

ID X24977 standard; cDNA; 942 BP.

XX AC X24977;

XX DT X24977;

XX 05-JUL-1999 (first entry)

XX DE Mouse TRAIN-R (long form) cDNA.

XX

KW TRAIN-R; receptor; mouse; tumour necrosis factor receptor;
KW agonist; antagonist; cancer; immunological disease; therapy;
KW cytostatic; ss.

XX Mus musculus.

XX Key Location/Qualifiers
FH 101..745
FT CDS
FT /*tag= a

XX

XX W09913078-A1.

XX 18-MAR-1999.

XX

XX 11-SEP-1998; 98WO-US19030.

XX 06-MAY-1998; 98US-0084422.

XX 12-SEP-1997; 97US-0058631.

XX (BIOJ) BIOGEN INC.

XX Hession C, Tschopp J;

XX WPI; 1999-229238/19.

XX P-PSDB; W98145.

XX

XX New cysteine-rich tumor necrosis factor receptor

XX Claim 1; Page 26-27; 30pp; English.

XX

XX The present sequence encodes a novel murine cysteine-rich tumour

XX necrosis factor receptor family member termed TRAIN-R (long form)

XX (see W98145). Murine TRAIN-R is expressed at high levels in brain

XX and lung, and at lower levels in liver, skeletal muscle and kidney.

XX Cell death can be induced by administering an agent capable of

XX inhibiting the binding of TRAIN-R to its ligand. A claimed method

XX of treating, or reducing, the advancement, severity or effects of

XX an immunological disease in a mammal comprises administering a

XX pharmaceutical composition which comprises a TRAIN-R blocking agent,

XX e.g. soluble TRAIN-R (see also W98144). TRAIN-R can be fused to an

XX immunoglobulin molecule to produce a fusion protein which may be

XX targeted to various sites. It can be used in binding assays, and

XX to identify antagonists and agonists. Anti-TRAIN-R receptor

XX antibodies can be used to reduce the severity of an immune response

XX or to treat cancer. TRAIN-R blocking agents can be used to reduce

XX the severity or effects of an immunological disease (all claimed).

XX

XX Sequence 942 BP; 219 A; 264 C; 258 G; 200 T; 1 other;

XX

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PF	27-JAN-1999;	99WO-US01679.
XX		
PR	27-JAN-1998;	98US-0014195.
PA		
XX	(MILL-) MILLENNIUM BIOTHEAPEUTICS INC.	
PI	Busfield SJ;	
XX		
XX	WPI; 1999-458707/38.	
DR	P-PSDB; Y06522.	
DR		
XX		
PT	New STRIFEI and STRIFEII polypeptides, proteins and nucleic acid	
PT	molecules useful for modulating TNFR associated disorders	
XX		
XX	Claim 3; Fig 1A-B; 119pp; English.	
XX	This is the nucleotide sequence of mouse STRIFE1 (also called	
CC	Tango 127a or Tl27a) cDNA. It encodes a protein (see Y05422) that	
CC	belongs to the tumour necrosis factor receptor (TNFR) superfamily.	
CC	2 Splice forms of murine STRIFE have been identified, one that is	
CC	predicted to be membrane-bound (STRIFE1) and one that is secreted	
CC	(STRIFE2, see Y06523). STRIFE was identified as a TNFR homologue	
CC	by a computer-based search of public EST databases. The invention	
CC	provides STRIFE1 and STRIFE2 polynucleotides and polypeptides, as	
CC	well as fusion proteins, antigenic peptides and antibodies. It	
CC	also provides expression vectors, host cells and transgenic	
CC	animals, as well as diagnostic, screening and therapeutic methods.	
CC	STRIFE I and STRIFE II may play a role in mediating inflammatory,	
CC	immune and host defense functions and may play a role in various	
CC	neoplastic disease states. They may be useful as targets for	
CC	developing novel diagnostic and therapeutic agents for TNF- and	
CC	TNFR-associated disorders. Examples include sepsis syndrome,	
CC	circulatory collapse and shock resulting from bacterial infection,	
CC	acute and chronic parasitic or infectious processes, acute and	
CC	chronic immune and autoimmune pathologies, alcohol-induced	
CC	hepatitis, chronic inflammatory pathologies, vascular inflammatory	
CC	pathologies, graft-versus-host pathology, malignant pathologies	
CC	involving TNF-secreting tumors, cerebral malaria and multiple	
CC	sclerosis.	
XX		
SQ	Sequence 981 BP; 247 A; 270 C; 264 G; 200 T; 0 other;	
Query Match 27.0%; Score 460.8; DB 20; Length 981;		
Best Local Similarity 81.9%; Pred. No. 6.8e-134;		
Matches 531; Conservative 0; Mismatches 117; Indels 0; Gaps		
QY	22	aataatacatttgataaagaagattgctttaaaagtgctactagacaagaagaaaacgt 81
Db	84	aataaacacgtttgtgagagcatggtcactcaagtgctctacctctacacgagcgtgc 143
QY	82	ttttcactcttttagtattactaggctattttgctatgaagtgcacttgtaaacaggag 141
Db	144	tcttcgtcgcatctctctcctcctccacctggcagtgaagtgtggtgcgaaccggag 203
QY	142	actgtagacagcaagaattcaggagatcggtctggaacctgtgtccctgcacaaccagtgtg 201
Db	204	atgacggcagcaggaattcaagatcgatctggaacctgtgctctgcaaacagtgcg 263
QY	202	ggccaggcatggagttgtctaaggaattggtctcggtatggggaggagatgcacagtgtg 261
Db	264	gacctggcatggagttgtccaaggaattggtctcggtatggggaggagatgcacagtgtg 323
QY	262	tgacgtgcggctgcacaggtttcaagaggactggggcttccagaataatgcaagccctgtc 321
Db	324	tgccttcgagccgcacgggtttcaagaaagactgggggtttcccaagagttgaagccatgtg 383
QY	322	tggactcgcgactggtgaaccgctttcaagaaggcaaatgttccagccaccagtgtgcga 381
Db	384	cgactgtgcgctggtgaaccgctttcagaaggggccaactgctcacacaccagtgtgtctg 443
QY	382	tctcgggggactgcttgccaggattttataggaagacgaaactgtctcgctttccaagaca 441

DE Mouse NTR-5 cDNA.
KW NTR-5; mouse; receptor; signal transduction; bone; muscle;
KW diagnosis; therapy; ss.
XX
OS Mus musculus.

FH Key Location/Qualifiers
FT CDS 3..485
TT /*tag= a

XX WO9933967-A2.

XX 08-JUL-1999.

XX 28-DEC-1998; 98WO-US27688.

XX 29-DEC-1997; 97US-0068925.

XX (REGE-) REGENERON PHARM INC.

XX Valenzuela DM;

XX WPI; 1999-419102/35.

XX P-PSDB; Y06399.

XX New mammalian receptor NTR-5 polypeptides

XX Example 1; Page 19; 27pp; English.

XX This is the nucleotide sequence of murine cDNA coding for a novel
CC receptor, designated NTR-5 (see Y06399), that shows homology to
CC osteoprotegerin and tumour necrosis factor (TNF) receptor. 2 cDNA
CC clones containing the present sequence were isolated following an
CC EST database search using human and mouse TNF family members as
CC query sequences. The murine NTR-5 cDNA was used as a probe in
CC the isolation of human NTR-5 cDNA (see X59346). Homology to
CC osteoprotegerin suggests that NTR-5 is involved in the regulation
CC of bone mass, and may be useful for regulating development,
CC proliferation and death of osteoblast or osteoclast cells or for
CC regulating muscle metabolism, and that it may be implicated in
CC muscle diseases or disorders. A host-vector system for production
CC of NTR-5 is claimed. NTR-5 polypeptides can be used as immunogens
CC and in screening assays to identify NTR-5 ligands, agonists and
CC antagonists. The NTR-5 polynucleotide is useful as a diagnostic
CC tool, and as a source of probes and primers. The invention also
CC provides for diagnostic and therapeutic methods based on the
CC interaction of NTR-5 and agents that initiate signal transduction
CC through binding to NTR-5.

XX Sequence 538 BP; 111 A; 153 C; 152 G; 122 T; 0 other;

XX
XX
XX Query Match 21.3%; Score 362.6; DB 20; Length 538;
XX Best Local Similarity 86.2%; Pred. No. 2.5e-103;
XX Matches 401; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 205 caggcatgagttgttaaggagtggtctcgctcgtatgggagagtgacacagtggtga 264

DB 1 ctggcagtgagttgtccaaggagtggtctcgctcgtatgggagagtgacacagtggtgc 60

QY 265 cgtgcggctgcacaggttcaaggagtggtcggcttcagaaatgcagaccctgtctgg 324

DB 61 cctgcagcgcacccggttcaaggagtggtcggcttcagaaatgcagaccctgtctgg 120

QY 325 actgcgcagtggtgaaccgctttcagaaggaatgttcagccaccagtgatgcacatc 384

DB 121 actgtgcgtgtgaaccgctttcagaaggaatgttcagccaccagtgatgcacatc 180

QY 385 gcggggactgctgcagagatttataggaagacgaactgtcggctttcaagacatgg 444

DB 181 gcggggactgctgcagagatttatccgggaagacgaactgtcggctttcaagacatgg 240

QY 445 agtgtgtgctgttgagagaccctctctcttaccagaccgactgtgcacgaagtga 504
DB 241 agtgtgtgctgttgagagaccctctctcttaccagaccgactgtgcacgaagtga 300
QY 505 acctcgtgaagatcgctccacggcctccagccacggagacacggcgtggtgcggtta 564
DB 301 accttgtgaagattctctccacgctctccagccctcggacacggcgtggtgcggtta 360
QY 565 tctgcagcgtctgcccaccgctcctcgtggtccctcgtcctcctcgtcactctattga 624
DB 361 tctgcagcgtctgcccaccgctcctcgtggtccctcgtcctcctcgtcactctactga 420
QY 625 agagacagtttatggagaagaaccacccagctggtctctcgtcgtgcac 669
DB 421 agaggcagttcatggagaagaaccacccagctgtaagctccatccc 465

RESULT 13

V11422

ID V11422 standard; cDNA; 371 BP.

XX AC V11422;

XX DT 23-JUL-1998 (first entry)

XX Human secreted protein clone AX92_3 cDNA 5'-end.

XX Secreted protein; prevention; treatment; gene therapy; ds.

XX Homo sapiens.

XX WO9801554-A2.

XX PD 15-JAN-1998.

XX PF 07-JUL-1997; 97WO-US11876.

XX PR 09-JUL-1996; 96US-0677231.

XX PA (GENY) GENETICS INST INC.

XX PI Bowman M, Evans C, Jacobs K, LaVallie ER, McCoy JM;

XX PI Merberg D, Racie LA, Spaulding V, Treacy M;

XX DR WPI; 1998-110230/10.

XX DR P-PSDB; W58844.

XX PT Secreted proteins and polynucleotides encoding them - useful to

XX PT prevent, treat and ameliorate medical conditions

XX PS Claim 15; Page 57; 93pp; English.

XX V11422-V11424 encode fragments of a novel secreted protein derived from
CC clone AX92_3 which was isolated from a human adult testes cDNA library.
CC The protein can be used to prevent, treat or ameliorate a medical
CC condition, while the polynucleotides can be used for gene therapy.

XX Sequence 371 BP; 83 A; 96 C; 107 G; 82 T; 3 other;

XX
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XX Best Local Similarity 98.1%; Pred. No. 4e-103;
XX Matches 364; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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 Db 361 ccagccacgg 371
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 AC
 AC X23417;
 DT 18-JUN-1999 (first entry)
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 XX Mouse mAPO4-gamma DNA.
 DE
 XX Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
 KW developmental abnormality; gestational abnormality; prostate cancer;
 APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
 KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
 KW apoptosis; mouse; APO4-gamma; ss.
 XX
 OS Mus sp.
 XX
 XX Key Location/Qualifiers
 FH 95..547
 FT CDS /tag- a /product- "mAPO4-gamma"
 FT
 XX WO9911791-A2.
 PN
 PD 11-MAR-1999.
 XX
 PF 04-SEP-1998; 98WO-US18393.
 XX
 PR 05-SEP-1997; 97US-0924634.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 XX Chaudhary PM;
 PI
 XX WPI; 1999-205191/17.
 -DR P-PSDB; W93583.
 DR
 XX New Tumor Necrosis Factor family receptor polypeptides and ligands -
 PT useful for diagnosis and treatment of prostate cancer and
 PT developmental or gestational abnormalities
 PT
 PS Disclosure; Fig 7E; 156pp; English.
 XX
 CC This invention describes isolated Tumor Necrosis Factor (TNF) family
 CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
 CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
 CC their active fragments. APO4 is useful for diagnosing prostate cancer
 CC by determining levels of APO4 in an individual. Prostate cancer can also
 CC be treated using APO4 selective binding agents linked to a therapeutic
 CC moiety. APO4 polypeptides are also useful for identifying selective
 CC binding agents, useful in diagnosis/treatment of disease by binding of
 CC agents to the polypeptide/active fragment which is extracellular, or

CC expressed on the cell surface. The binding is preferably performed in
 CC vivo. APO4 polypeptides/ active fragments are also useful for screening
 CC for agonists and antagonists by binding and observing the change in APO4
 CC activity. Effective pharmacological agents useful in diagnosis or
 CC treatment of disease are also identified using APO4 polypeptides/active
 CC fragments and APO4 signal transducer molecules that specifically interact
 CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
 CC activity. The method is performed in vivo or in vitro. APO polypeptides
 CC are all useful as immunogens for preparing antibodies. APO4 is also
 CC useful for diagnosis/treatment of developmental or gestational
 CC abnormalities. APO8 was transfected to human breast carcinoma cell line
 CC MCF-7, and induced apoptosis.
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 SQ Sequence 591 BP; 148 A; 145 C; 175 G; 123 T; 0 other;
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 Best Local Similarity 78.2%; Pred. No. 4.8e-92;
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 QY 78 acgtttttcactcttttagtattactaggtctatttgcattgtaaaagtgttccctgcaaccag 137
 Db 128 gtgctcttcgctccattctcttctactcaccctggcatgtaaaagtgttgcgaacc 187
 QY 138 ggaagactgttagacagaagaattcaggatcggtctggaacctgttccctgcaaccag 197
 Db 188 ggaagattcgaggcagcagggaattcaaggatcgatctggaacctgttccctgcaaccag 247
 QY 198 tgggcccagcagtgatgtgttaaggaatgtgcttcgctatgggagagatgcacag 257
 Db 248 tgcggacctggtgagtggttgcacagggaatgtggtctcggtatggggaggtgcacag 307
 QY 258 tgtgtgactgcccggctgcacaggttcaaggagactggggtctccagaaatgcaagccc 317
 Db 308 tgtgtgacctgcaggccgcacccggttcaaggaaagactggggttccagaaagttaagcca 367
 QY 318 tgtctggaactgcgactggtggaacctcttcagaagcaaaatgttcaagccacagtgat 377
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 DT 05-JUL-1999 (first entry)
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 DE Mouse TRAIN-R (short form) cDNA.
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 KW TRAIN-R; receptor; mouse; tumour necrosis factor receptor;
 KW agonist; antagonist; cancer; immunological disease; therapy;
 KW cytostatic; ss.
 XX
 OS Mus musculus.
 XX

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 12:32:29 ; Search time 217.59 Seconds
(without alignments)
1262.085 Million cell updates/sec

Title: US-09-380-276A-2

Perfect score: 1704

Sequence: 1 gggaacgtagaactccaa.....gaccacagatatttttc 1704

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 280836 seqs, 80580151 residues

Total number of hits satisfying chosen parameters: 561672

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	36.4	2.1	1987	1 US-08-722-001-26	Sequence 26, Appl
3	36.4	2.1	1997	1 US-08-722-001-27	Sequence 27, Appl
4	36.4	2.1	2004	1 US-08-722-001-11	Sequence 11, Appl
5	36.2	2.1	2485	1 US-08-424-424B-1	Sequence 1, Appli
6	36.2	2.1	2486	4 PCT-US94-05363A-1	Sequence 1, Appli
7	35.4	2.1	7218	1 US-08-232-463-14	Sequence 14, Appl
8	34.8	2.0	1639	1 US-08-334-698-5	Sequence 5, Appli
9	34.8	2.0	1639	1 US-08-228-932-5	Sequence 5, Appli
10	34.8	2.0	1639	1 US-08-468-939-5	Sequence 5, Appli
11	34.8	2.0	1639	2 US-08-406-855A-5	Sequence 5, Appli
12	34.8	2.0	1639	3 US-08-722-190-5	Sequence 5, Appli
13	34.8	2.0	1639	3 US-08-244-354-5	Sequence 5, Appli
14	34.8	2.0	1639	3 US-09-206-899-5	Sequence 5, Appli
15	34.8	2.0	1639	4 PCT-US95-04203-5	Sequence 5, Appli
16	34.6	2.0	5962	5 5386025-5	Patent No. 5386025
17	33.6	2.0	800	2 US-08-416-603-11	Sequence 11, Appl
18	33.4	2.0	4360	1 US-08-470-350B-1	Sequence 1, Appli
19	33	1.9	9472	1 US-08-325-547-9	Sequence 9, Appli
20	32.8	1.9	2230	1 US-08-200-512-1	Sequence 2, Appli
21	32.6	1.9	1593	2 US-08-524-828-2	Sequence 2, Appli
22	32.6	1.9	1593	2 US-08-975-114A-2	Sequence 2, Appli
23	32.6	1.9	1593	3 US-08-849-281A-2	Sequence 2, Appli
24	32.6	1.9	2247	2 US-08-524-828-1	Sequence 1, Appli
25	32.6	1.9	2247	2 US-08-975-114A-1	Sequence 1, Appli
26	32.6	1.9	3891	1 US-08-480-604A-27	Sequence 27, Appl
27	32.6	1.9	3891	1 US-08-405-496A-27	Sequence 27, Appl
28	32.4	1.9	1167	1 US-07-960-985-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-722-001-7
; Sequence 7, Application US/08722001
; Patent No. 5760054
; GENERAL INFORMATION:
; APPLICANT: Thompson, Wayne J.
; APPLICANT: Huff, Joel R.
; APPLICANT: Nerenberg, Jennie B.
; APPLICANT: Lee, Hee-Yoon
; APPLICANT: Bell, Ian M.
; TITLE OF INVENTION: ALPHALIC ADRENERGIC RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,001
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/229,276
; FILING DATE: 14-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Appollina, Mary A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19169Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-722-001-7

Sequence 1, Appli
Sequence 3, Appli
Sequence 36, Appli
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Sequence 1, Appli

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Best Local Similarity 52.7%; Pred. No. 0.31;
Matches 79; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

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QY 578 ggcacccgtctcgtggcctgctcatctctgtgtcatctattgaaagacaggtttat 637
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DB 1167 GGGCTCTCTTACCTGCCCTTGGCCATCATCTGCTCATGTACTGCCGCGTCTAGTGGT 1226

QY 638 gagagaagaacccagctggtctctcgcggtc 667
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DB 1227 GGCCAAAGAGGAGAGCGGGGCGCTCAAGTC 1256

RESULT 2
US-08-722-001-26
; Sequence 26, Application US/08722001
; Patent No. 5760054
; GENERAL INFORMATION:
; APPLICANT: Thompson, Wayne J.
; APPLICANT: Huff, Joel R.
; APPLICANT: Nerenberg, Jennie B.
; APPLICANT: Lee, Hee-yoon
; APPLICANT: Bell, Ian M.
; TITLE OF INVENTION: ALPHAIC ADRENERGIC RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,001
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/229,276
; FILING DATE: 14-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Appollina, Mary A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19169Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1987 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-722-001-26

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Matches 79; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

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RESULT 11
US-08-406-855A-5
; Sequence 5, Application US/08406855A
; Patent No. 5861309
; GENERAL INFORMATION:
; APPLICANT: Jonathan A. Bard et al.
; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
; TITLE OF INVENTION: Receptors and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,855A
; FILING DATE: 21-AUG-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KDB

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RESULT 12
US-08-722-190-5
Sequence 5, Application US/08722190
Patent No. 5990128
GENERAL INFORMATION:
APPLICANT: Charles Gluchowski, Carlos C. Forray, George
APPLICANT: Chiu, Theresa A. Branchek, John M. Wezel and Paul R. Hartig
TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
TREAT BENIGN PROSTATIC HYPERPLASIA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,190
FILING DATE: 4-APR-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878-D-PCT/JPW/AGL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1639 base pairs


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1  SINGLE SOURCE NUMBER: 26.000
2  REFERENCE/DOCKET NUMBER: 41337-A-PCIT-US/JPW/KDB
3  TELECOMMUNICATION INFORMATION:
4  TELEPHONE: (212) 278-0400
5  TELEFAX: (212) 391-0526
6  INFORMATION FOR SEQ ID NO: 5:
7  SEQUENCE CHARACTERISTICS:
8  LENGTH: 1639 base pairs
9  TYPE: nucleic acid
10 STRANDEDNESS: single
11 TOPOLOGY: unknown
12 MOLECULE TYPE: DNA (genomic)
13 HYPOTHETICAL: N
14 ANTI-SENSE: N
15 FEATURE:
16 NAME/KEY: CDS
17 LOCATION: 126..1523
18 OTHER INFORMATION:
19 US-09-206-899-5

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

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Total number of hits satisfying chosen parameters: 2236266

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Maximum DB seq length: 2000000000

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ALIGNMENTS

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ACCESSION AB040434
VERSION AB040434.1 GI:9392329
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SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (sites)
Kojima,T., Morikawa,Y., Copeland,N.G., Gilbert,D.J., Jenkins,N.A.,
Senba,E. and Kitamura,T.
TROY, a newly identified member of the tumor necrosis factor
receptor superfamily, exhibits a homology with Edar and is
expressed in embryonic skin and hair follicles
J. Biol. Chem. 275 (27), 20742-20747 (2000)
2037167
2 (bases 1 to 1364)
Kojima,T. and Kitamura,T.
Direct Submission
Submitted (23-MAR-2000) to the DDBJ/EMBL/GenBank databases. Tetsuo
Kojima, Chugai Research Institute for Molecular Medicine, Inc.,
Cytokine Research Program, 153-2 Nagai, Nihari, Ibaraki 300-4101,
Japan (E-mail:kojimat@clmmed.com, Tel:81-298-306211,
Fax:81-298-306270)
Sequence updated (06-Apr-2000).
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1266; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 421 cctctcctctcttaagacgaactgtgcagcaaggttcaacctctgaagatcgcgttc 480
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QY 481 aaggcctccagccacgggacacggcgctggctgcgttatctgcagcctctggccacc 540
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QY 841 aacgcaggccacggcgaggagatgggtgcgaccttcttcggaacctccctcagcagctccatc 900
Db 877 AAGCGAGCCACGACCCGGGAGAGTGTGGCGACTTCTTCTCGGATCCCTCAGCGAGTCCATC 936
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Qy 1261 ggttccctg 1269
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RESULT 2
AF167555 AF167555 1489 bp mRNA PRI 25-MAY-2000
LOCUS Homo sapiens TAJ-alpha mRNA, complete cds.
DEFINITION AF167555
ACCESSION AF167555
VERSION AF167555.1 GI:8071643
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1489)
AUTHORS Eby,M.T., Jasmin,A., Kumar,A., Sharma,K. and Chaudhary,P.M.
TITLE TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
Activates the c-Jun N-terminal Kinase Pathway and Mediates
Caspase-Independent Cell Death
J. Biol. Chem. 275 (20), 15336-15342 (2000)
10809768
JOURNAL PUBMED
2 (bases 1 to 1489)
AUTHORS Chaudhary,P.M.
TITLE Direct Submission
JOURNAL Submitted (12-JUL-1999) Internal Medicine, UT Southwestern Medical
Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8593, USA
FEATURES
Location/Qualifiers
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ORIGIN

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Query Match 99.0%; Score 1256.2; DB 37; Length 1489;

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Best Local Similarity 99.4%; Pred. No. 0;
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Db 785 TCAGTGCAGACCTTGGGCGCGGTGCGCTGTCTCCCATCATGTGTGTGTGAGAGGCGCTGC 844
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Db 1205 ACTAGGTAGAAATCAGCATCACTCAGGATGCCTAACTAACTATGAGAGCCAGCTAGATCAG 1264

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Db 1325 GGTTCCTCGT 1333

RESULT 3

AB040432 3964 bp mRNA ROD 22-JUL-2000

LOCUS Mus musculus mRNA for TROY, complete cds.

DEFINITION AB040432

ACCESSION AB040432.1 GI:9392325

VERSION

KEYWORDS TROY.

SOURCE Mus musculus cDNA to mRNA.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Senba, E. and Kitamura, T.

TITLE TROY, a newly identified member of the tumor necrosis factor receptor superfamily, exhibits a homology with Edar and is expressed in embryonic skin and hair follicles

JOURNAL J. Biol. Chem. 275 (27), 20742-20747 (2000)

MEDLINE 20347167

REFERENCE 2 (bases 1 to 3964)

AUTHORS Kojima, T., Morikawa, Y., Copeland, N.G., Gilbert, D. J., Jenkins, N.A., Senba, E. and Kitamura, T.

TITLE TROY, a newly identified member of the tumor necrosis factor receptor superfamily, exhibits a homology with Edar and is expressed in embryonic skin and hair follicles

JOURNAL Submitted (23-MAR-2000) to the DDBJ/EMBL/GenBank databases. Tetsuo Kojima, Chugai Research Institute for Molecular Medicine, Inc., Cytokine Research Program; 153-2 Nagai, Nihari, Ibaraki 300-4101, Japan (E-mail: kojima@climmed.com, Tel:81-298-306211, Fax:81-298-306270)

FEATURES

Location/Qualifiers

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BASE COUNT 984 a 958 c 980 g 1041 t 1 others

ORIGIN

Query Match 57.7%; Score 732.4; DB 11; Length 3964;

Best Local Similarity 74.8%; Pred. No. 3.5e-187;

Matches 932; Conservative 0; Mismatches 311; Indels 3; Gaps 1;

QY 1 atgctttaaagtgtactagaaagaagaaaaacgttttttcaactcttttagtattacta 60

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QY 61 ggtatttgcattgaagtgtctgtgaaacagggagactgtagacagcaagaattcagg 120

Db 187 CTCACCTGCGATGTAAAGTGAGTTGGGAAACCGGAGATTGCAGGACGAGGAATTCAG 246

QY 121 gatcgcttggaaactgtgtcccttcaaccagctgtgggcccagggcatggagttgtttaag 180

Db 247 GATCGATCTGGAACCTGTGTCTCTGCAACAGTGCAGGACCTGCCATGGAGTTGTCCAAG 306

QY 181 gaatggtgttcggtcatgtgggagagatgcacagctgtgtgacgtgcccgtgcacaggttc 240

Db 307 GAATGTGGCTTCGGCTATGGGAGGATGCACAGTGTGCCCCGACAGCGCCACCGGTT 366

QY 241 aaggagactggggtctccagaaaatgcaagccctgtctggaactgcgagtggtgaaaccgc 300

Db 367 AAGGAAGACTGGGGTTTCCAGAAAGTGTAAAGCAATGTCCGAGACTGTGGCTGGTGAACCG 426

QY 301 ttccagaagggcaaatgttccagccaccagtgatgccatctgcgggactgttgcaggga 360

Db 427 TTTTCAGAGGGCCAACTGCTCACACACAGTGTCTGTGCGGGGACTGCCGTGCCAGGA 486

QY 361 ttattatagaagcgaactgttcggtcttcaagacacatggagtggtgcttggagac 420

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Db 907 AGTCTGCCCGAGCTGTGCTTGGCTGTGGGCTGGGTTCTCCCACTACCCCTTCAGGAGAGA 966

QY 841 aacgcaggcccccagccggggagatggtgtccgacttttcggatccctcacgagttccatc 900

Db 967 AACCCGGCTTCTGTGGGGACAGATGCCACGCTTCTTCGGGTCTGTTCCTCCGCTTCCATC 1026

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QY 961 tcttttgcactcttctcgaactcactcagtcaggaagacattcatctctcaatccagaa 1020

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QY 1021 cttgaaagctcaacgtcttcttggattcaaaatagcagctcaagatttgggtggtgggctgtt 1080

Japan (E-mail:kojimat@immed.com, Tel:81-298-306211,
Fax:81-298-306270)

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FEATURES
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Best Local Similarity 82.4%; Pred. No. 1.5e-110;
Matches 515; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

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Qy 61 ggcatttgcattgaagtgaactgtgaacacagagagactgaacacagaattcagg 120
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Qy 121 gatcggtctgaaactgttctccctgcaacagtggtggccaggcatggagtgtctctaa 180
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Db 187 GATCGATCTGGAACATGTGTCTCTGCAACACAGTCGCGGACCTGGCATGGAGTTGTCCAAG 246

Qy 181 gaatgtgcttgaggctatggggaggatgcacagtggtgagctgagcgcgctgcacagg 240
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Db 247 GAATGTGCTTCGGGTATGGGAGAGATGCACAGTGTGTGCCCTGCGGCGCACCGCGTTC 306

Qy 241 aaggaggactgggcttcagaaatgcagccctctctgagctgcgagtggtgaaccgc 300
   ||||| || || || || || || || || || || || || || || || || || || ||
Db 307 AAGGAGACTGGGGTTTCAGAAAGTGTAAAGCATGTGCGGACTGTGCGTGTGTAACCGC 366

Qy 301 ttccagaaggcaaatgtttcagccaccagtgatgccatctctggggagctgcttgcagg 360
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Db 487 CCACCTCTCTCTACGACCACTGTACACAGCAGAGTGAACCTGTGAAGATCTCTCTCC 546

Qy 481 acggcctccagcccaaggagacggcgctggctgcgttatctgagcgcgttggccacc 540
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Db 607 GTGCTGTGCGCCCTGCTCATCTGTGTGTATCTACTCAAGAGCGCATCTCATGAGAAG 666

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RESULT 7

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LOCUS      Mus musculus TAU-alpha short mRNA, complete cds.
DEFINITION      AF167553
ACCESSION      AF167553
VERSION      AF167553.1 GI:8071639
KEYWORDS
SOURCE      house mouse.
ORGANISM      Mus musculus
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              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 886)
AUTHORS      Eby,M.T., Jasmin,A., Kumar,A., Sharma,K. and Chaudhary,P.M.
TITLE      TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
              Activates the c-Jun N-terminal Kinase Pathway and Mediates
              Caspase-Independent Cell Death
JOURNAL      J. Biol. Chem. 275 (20), 15336-15342 (2000)
PUBMED      10809768
REFERENCE      2 (bases 1 to 886)
AUTHORS      Chaudhary,P.M.
TITLE      Direct Submission
JOURNAL      Submitted (12-JUL-1999) Internal Medicine, UT Southwestern Medical
              Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8593, USA
FEATURES
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BASE COUNT  204 a 245 c 247 g 190 t
ORIGIN
Query Match      35.4%; Score 449; DB 11; Length 886;
Best Local Similarity 82.4%; Pred. No. 1.5e-110;
Matches 515; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

Qy 1 atggtttaaagtgtctactagaacagagaaacgcttttctactcttttagtattacta 60
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Db 72 ATGGGACTCAAGGTCCTACCTCTACACAGGAGCGGTCTCTTCGCTGCCATCTCTCTCTA 131

Qy 61 ggcatttgcattgaagtgaactgtgaacacagagagactgaacacagaattcagg 120
   ||||| || || || || || || || || || || || || || || || || || || ||
Db 132 CTCCACCTGGCATGTAAAGTAGTTGCGAAACCGGAGATGTCAGGACGAGAAATTCAG 191

Qy 121 gatcggtctgaaactgttctccctgcaacagtggtggccaggcatggagtgttctaa 180
   ||||| || || || || || || || || || || || || || || || || || || ||
Db 192 GATCGATCTGGAACATGTGTCTCTGCAACACAGTCGCGGACCTGGCATGGAGTTGTCCAAG 251

Qy 181 gaatgtgcttgaggctatggggaggatgcacagtggtgagcgtgcgcagaggttc 240
   ||||| || || || || || || || || || || || || || || || || || || ||
Db 252 GAATGTGCTTCGGGTATGGGAGAGATGCACAGTGTGTGCCCTGCGGCGCACCGCGTTC 311

Qy 241 aaggaggactgggcttcagaaatgcagccctcgtctggagctgcgagtggtgaaccgc 300
   ||||| || || || || || || || || || || || || || || || || || || ||
Db 312 AAGGAAGACTGGGGTTTCCAGAAAGTGTAAAGCATGTGCGGACTGTGCGTGTGTAACCGC 371

Qy 301 ttccagaaggcaaatgtttcagccaccagtgatgccatctcggggagctgcttgcagg 360
   ||||| || || || || || || || || || || || || || || || || || || ||
Db 372 TTTCAGAGGGCCAACTGTCTCACACACAGTGTGTGTCTGCGGGGACTGCTGTCCAGGA 431

Qy 361 ttttataagaagacaaactgtcggcttcaagacatggagtggtgcttggtagagac 420
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Db 432 TTTTACGGGAACCAAACTGTTGGTTTTTCAAGACATGAGTGTGTGCCCTCGGAGAC 491
 QY 421 cctccctcttaccagcactgtccagcaaggtcaacctctggaagatcgcgtcc 480
 Db 492 CCACCTCTCTTACCAACCACTGTACCAAGGAGTGAACCTGTGAAGATCTCCTCC 551
 QY 481 acgctctcagccagcgggacagcgctgtggtgctgtatctgcagcgtctctggccacc 540
 Db 552 ACCGTCTCCAGCCTCGGGACACGGCGTGGCTGCGCTCATCTGCAGTGTCTGGCCACG 611
 QY 541 gtctctgtgcccctgtctatctctctgtgtctatctgttaagagacagttatggagaag 600
 Db 612 GTCTGTCTGCCCCGTCTCATCTGTGTGTCTCATCTACTGCAAGAGGAGTTTCATGGAGAAG 671
 QY 601 aaaccagctggtctctgcggtcac 625
 Db 672 AAACCCAGCTGTAAAGTCCCATCCC 696

RESULT 8
 AL161422
 LOCUS Homo sapiens chromosome 13 clone RP11-168G12, HTG 20-SEP-2000
 DEFINITION
 ACCESSION AL161422
 VERSION
 KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 143608)
 Pearce.A.
 Direct Submission
 Submitted (19-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 requests: clonerequest@sanger.ac.uk
 On Sep 22, 2000 this sequence version replaced gi:10190601.
 ----- Genome Center
 Center: Sanger Centre
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: humquery@sanger.ac.uk
 ----- Project Information
 Center project name: BA168G12
 ----- Summary Statistics
 Assembly program: XGAP4; version 4.5
 Sequencing vector: pLasmid; L08752; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Consensus quality: 143007 bases at least Q40
 Consensus quality: 143260 bases at least Q30
 Consensus quality: 143347 bases at least Q20
 Insert size: 143408; sum-of-contigs
 Insert size: 145175; 5.9% error; agarose-fp
 Quality coverage: 8.55x in Q20 bases; sum-of-contigs Quality
 coverage: 8.58x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 3 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 2992: contig of 2992 bp in length
 * 2993 3092: gap of 100 bp
 * 3093 129375: contig of 126283 bp in length
 * 129376 129475: gap of 100 bp
 * 129476 143608: contig of 14133 bp in length.
 * Location/Qualifiers
 * 1 .143608
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FEATURES
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 200 others
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 Query Match 33.8%; Score 428.8; DB 67; Length 143608;
 Best Local Similarity 99.5%; Pred. No. 4.9e-105;
 Matches 430; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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 QY 898 atctgtggcgagttttcagatgcctgtggcctctgatgcagaatcccccaggtggtgacaac 957
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 Db 84933 ATCTCTTTTGTGACTCTTATCTGAACCTGAGTGGAGAGACATTCATCTCTCAATCCA 84992
 QY 1018 gaactggaagctcaacgtcttttggattcaaatagcagtcgaagattgtgttggggct 1077
 Db 84993 GAACTTGAAGCTCAACAGCTTTTGGATTCAAAATAGCAGTCAAGATTGTGTGGGGCT 85052
 QY 1078 gtccagtcagctctattctgaaaaactttacagcagctactgattctatctagataaac 1137
 Db 85053 GTTCCAGTCCAGTCTCTTCTGAAAACCTTTACAGCAGTACTGATTTTCTAGATATAAC 85112
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 Db 85113 AACACACTGGTAGAATCAGCATCACTCAGGATGCATTAATATGAGAAGCCAGCTAGAT 85172
 QY 1198 caggagagtggtgctatcatccaccagccactcagacgtccctccaggttaaggcagcga 1257
 Db 85173 CAGGAGAGTGGTGTCTGTCATCCACCAGCCACTCAGACGTCCTCCAGGTAAAGCGAGA 85232
 QY 1258 ctgggttccctg 1269
 Db 85233 CTGGGTCCCTG 85244
 RESULT 9
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 LOCUS Homo sapiens chromosome 13 clone RP11-173N17 map q12.11-12.3, HTG 29-SEP-2000
 DEFINITION
 ACCESSION AL139080
 VERSION
 KEYWORDS HTG: HTGS_PHASE1; HTGS_DRAFT.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 178256)
 Burton.J.
 Direct Submission
 Submitted (28-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 requests: clonerequest@sanger.ac.uk

COMMENT

On Oct 1, 2000 this sequence version replaced gi:10129398.
 ----- Genome Center
 Center: Sanger Centre
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: humquery@sanger.ac.uk
 ----- Project Information
 Center project name: ba173n17
 ----- Summary Statistics
 Assembly program: XGAP4; version 4.5
 Sequencing vector: plasmid; 108752; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Consensus quality: 168976 bases at least Q40
 Consensus quality: 172107 bases at least Q30
 Consensus quality: 173780 bases at least Q20
 Insert size: 176856; sum-of-contigs
 Insert size: 163577; 8.6% error; agarose-fp
 Quality coverage: 3.73x in Q20 bases; sum-of-contigs Quality
 coverage: 4.07x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 15 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 8223: contig of 8223 bp in length
 * 8224 8323: gap of 100 bp
 * 8324 25426: contig of 17103 bp in length
 * 25427 25526: gap of 100 bp
 * 25527 28263: contig of 2737 bp in length
 * 28264 28363: gap of 100 bp
 * 28364 34273: contig of 5910 bp in length
 * 34274 34373: gap of 100 bp
 * 34374 42235: contig of 7862 bp in length
 * 42236 42335: gap of 100 bp
 * 42336 53917: contig of 11582 bp in length
 * 53918 54017: gap of 100 bp
 * 54018 71972: contig of 17955 bp in length
 * 71973 72072: gap of 100 bp
 * 72073 81711: contig of 9639 bp in length
 * 81712 81811: gap of 100 bp
 * 81812 88644: contig of 6833 bp in length
 * 88645 88744: gap of 100 bp
 * 88745 95048: contig of 6304 bp in length
 * 95049 95148: gap of 100 bp
 * 95149 107455: contig of 12307 bp in length
 * 107456 107555: gap of 100 bp
 * 107556 125465: contig of 17910 bp in length
 * 125466 125565: gap of 100 bp
 * 125566 140008: contig of 14443 bp in length
 * 140009 140108: gap of 100 bp
 * 140109 144761: contig of 4653 bp in length
 * 144762 144861: gap of 100 bp
 * 144862 178256: contig of 33395 bp in length.
 Location/Qualifiers
 1. 178256

FEATURES

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 72073. .81711
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 88745. .95048
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 140109. .144761
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 Best Local Similarity 99.5%; Pred. No. 4.9e-105;
 Matches 430; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 838 agaaacgcagccagccggggagatggtgcgcactttcttcggtatccctccacgcagtc 897
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 QY 898 atctgtggcagagtttcagatgcctgcctctgatgcagaatcccatgggtggtgacaac 957
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 QY 958 atctcttttgcactcttctgaactcactgcagagacattcattctctcaatcca 1017
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 QY 1018 gaacttgaagctcaacgtcttttgattcaaatagcagctcaagatttggtggtgggct 1077
 Db 46811 GAACCTGAAGCTCAACGCTCTTTGGATTCAATACAGTCAGTCAAGATTGGTTGGGGCT 46870
 QY 1078 gtccagctcagctctcatctctgaaacttacagcagctactgattctctagataaac 1137
 Db 46871 GTTCCAGTCCAGTCTCATCTCTGAAACTTTACAGCAGCTACTGATTATCTAGATATAAC 46930
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 Db 46931 AACACACTGGTAGAATCAGATCAACTCAGGATGCACCTAACTATGAGAAGCCAGCTAGAT 46990
 QY 1198 caggagagtggtgcgtatcatccaccaccgacctcagagctccctccaggttaaggcagga 1257
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 QY 1258 ctgggttcctcctg 1269

Db 47051 CTGGGTTCCCTG 47062

RESULT 10
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LOCUS Mus musculus TAJ-beta1 mRNA, complete cds.
DEFINITION AF167554
ACCESSION AF167554
VERSION AF167554.1 GI:8071641
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 591)
AUTHORS Eby,M.T., Jasmin,A., Kumar,A., Sharma,K. and Chaudhary,P.M.
TITLE TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
Activates the c-Jun N-terminal Kinase Pathway and Mediates
Caspase-independent Cell Death
J. Biol. Chem. 275 (20), 15336-15342 (2000)
PUBMED 10809768
REFERENCE 2 (bases 1 to 591)
AUTHORS Chaudhary,P.M.
TITLE Direct Submission
JOURNAL Submitted (12-JUL-1999) Internal Medicine, UT Southwestern Medical
Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8593, USA
FEATURES
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/db_xref="taxon:10090"
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95..547
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Query Match 24.7%; Score 314; DB 11; Length 591;
Best Local Similarity 78.9%; Pred. No. 4.8e-74;
Matches 374; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
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Db 95 ATGGCACTCAAGTCTACTCTACAGACAGCGGTGCTCTTCGCTGCCATTCTTCCTTA 154
QY 61 ggctattgtcattgaagtgacttggaaacaggagactgtatagacagcaagaattcagg 120
Db 155 CTCACCTGCGCATGTAAGTGAGTGTGCGAAACCGGAGATGTCAGGCGAGGAATTCAAG 214
QY 121 gatcgcttgaaactgtgttccctgcaaccagtgtggccaggcagtgagttgtctaaag 180
Db 215 GATCGATCTGGAACATGTGCTCTGCAACACAGTGGCGGACCTGGCATGGAGTTGTCCAAG 274
QY 181 gaatgtgcttcggctatggggaggatgcacagtgtgtgacgtgctggcgtgcacaggttc 240
Db 275 GAATGTGCTTCGCTATGGGAGGATGCACAGTGTGTGCCCTGTCAGGCGCACCGGTTTC 334
QY 241 aaggagactggggtctccagaataatgcaagccctgtctgtgactgcgcagtggtgaaccgc 300
Db 335 AAGGAAGACTGGGGTTTCCAGAAGTGTAAAGCCATGTGCGGACTGTGCGTGTGTGAACCGC 394
QY 301 ttcaagaagcaaatgttccagccaccagtgtgccatctgcgggagactgttgcaggga 360
Db 395 TTTCAGAGGGCCCAACTGCTCACACACACAGTGTGTCTGTGGGGGACTGCCGTGCCAGGA 454

QY 361 ttttataggagacgaactgtcgcttttcaagacatgagtggtgtgcttcttgagac 420
Db 455 TTTTACCGGAAGACCAACTGGTTGTTTTCAGACATGAGTGTGTGCGCTCGGAGAC 514
QY 421 cctctctcttctacgaacgcactgtgccagcaaggtcaacacctcgtgaagatc 474
Db 515 CCACCTCCTCCTTACGAACACACACTGTGAGTGATGTGCCAAGTGGCAGCAGAC 568
RESULT 11
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DEFINITION Homo sapiens chromosome X clone RP11-133K18, *** SEQUENCING IN
PROGRESS ***, 16 unordered pieces.
ACCESSION AL353136
VERSION AL353136.6 GI:9796991
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 188351)
AUTHORS Pavitt,R.
TITLE Direct Submission
JOURNAL Submitted (09-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
COMMENT On Aug 12, 2000 this sequence version replaced gi:9368011.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project information
Center project name: bA13K18
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 176827 bases at least Q40
Consensus quality: 181768 bases at least Q30
Consensus quality: 184650 bases at least Q20
Insert size: 186851; sum-of-contigs
Insert size: 162009; 18.4% error; agarose-fp
Quality coverage: 3.49x in Q20 bases; sum-of-contigs Quality
Coverage: 4.02x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 25437: contig of 25437 bp in length
* 25438 25537: gap of 100 bp
* 25538 27653: contig of 2116 bp in length
* 27654 27753: gap of 100 bp
* 27754 45836: contig of 18083 bp in length
* 45837 45936: gap of 100 bp
* 45937 58298: contig of 12362 bp in length
* 58299 58398: gap of 100 bp
* 58399 63898: contig of 5500 bp in length
* 63899 63998: gap of 100 bp
* 63999 70792: contig of 6794 bp in length
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* 83403 83502: gap of 100 bp
* 83503 112513: contig of 29011 bp in length
* 112514 112613: gap of 100 bp
* 112614 120587: contig of 7974 bp in length
* 120588 120687: gap of 100 bp

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6390 7655: contig of 1266 bp in length
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11239 13842: contig of 2584 bp in length
13823 13922: gap of 100 bp in length
13923 16968: contig of 3046 bp in length
16969 17068: gap of 100 bp
17069 20185: contig of 3117 bp in length
20186 20285: gap of 100 bp
20286 22634: contig of 2349 bp in length
22635 22734: gap of 100 bp
22735 27012: contig of 4278 bp in length
27013 27112: gap of 100 bp
27113 29342: contig of 2230 bp in length
29343 29442: gap of 100 bp
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33382 33481: gap of 100 bp
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36563 36662: gap of 100 bp
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40983 41082: gap of 100 bp
41083 45520: contig of 4438 bp in length
45521 45620: gap of 100 bp
45621 50623: contig of 5003 bp in length
50624 50723: gap of 100 bp
50724 55610: contig of 4887 bp in length
55611 55710: gap of 100 bp
55711 61038: contig of 5328 bp in length
61039 61138: gap of 100 bp
61139 66159: contig of 5021 bp in length
66160 66259: gap of 100 bp
66260 73479: contig of 7220 bp in length
73480 73579: gap of 100 bp
73580 80554: contig of 6975 bp in length
80555 80654: gap of 100 bp
80655 89313: contig of 8659 bp in length
89314 89433: gap of 100 bp
89414 98132: contig of 8719 bp in length
98133 98232: gap of 100 bp
98233 107469: contig of 9237 bp in length

*	107470	107569:	gap of	100 bp			
*	107570	117873:	contig of	10304 bp in length			
*	117874	117973:	gap of	100 bp			
*	117974	130973:	contig of	13000 bp in length			
*	130974	131073:	gap of	100 bp			
*	131074	143236:	contig of	12163 bp in length			
*	143237	143336:	gap of	100 bp			
*	143337	154478:	contig of	11142 bp in length			
*	154479	154578:	gap of	100 bp			
*	154579	169967:	contig of	15389 bp in length			
*	169968	170067:	gap of	100 bp			
*	170068	187347:	contig of	17280 bp in length			
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*	187448	205736:	contig of	18289 bp in length.			
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* 107570 117873: contig of 10304 bp in length
* 117874 117973: gap of 100 bp
* 117974 130973: contig of 13000 bp in length
* 130974 131073: gap of 100 bp
* 131074 143236: contig of 12163 bp in length
* 143237 143336: gap of 100 bp
* 143337 154478: contig of 11142 bp in length
* 154479 154578: gap of 100 bp
* 154579 169967: contig of 15389 bp in length
* 169968 170067: gap of 100 bp
* 170068 187347: contig of 17280 bp in length
* 187348 187447: gap of 100 bp
* 187448 205736: contig of 18289 bp in length.
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FEATURES

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1368..2402
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2503..3524
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3625..4913
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5014..6289
    /note="assembly_fragment"
6390..7655
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7756..9267
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9368..11138
    /note="assembly_fragment"
11239..13822
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13923..16968
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17069..20185
    /note="assembly_fragment"
20286..22634
    /note="assembly_fragment"
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misc_feature 89414..98132
    /note="assembly_fragment"

Query Match 5.2%; Score 65.4; DB 51; Length 205736;
Best Local Similarity 38.6%; Pred. No. 9.4e-07;
Matches 114; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

QY 179 agaatgtgtcttcctgcttgaggagatgcacagtggtgacgtgccggtcacaggt 238
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 154301 AGGAGAGTGGTATGGAGAGGTGGAGATGCCTACTGTGCAGAGACTGCTCCTCTCAGGT 154360

QY 239 tcaaggagactgggggtcttcagaaatgcaagccctgtctggactgcgagtggtgaacc 298
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 154361 ACACAAGCAGCTGGGGCCACACACATGTCAGAGATGCATCACCTGTGCTCATCAATC 154420

QY 299 gctttcagaagcaaatgttccagccaccagtgatgccatctcggggactgttccag 358
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 154421 GCGTTCACAAGGTGAATGCGCACATACCTCTTAATGCTGTGTGGGACTGTGTGCCNN 154480

QY 359 gattttataggagacgaaactgtctggtttcaagacatggagtggtgacctgtg99ag 418

Db 154481 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 154540

QY 419 acctctctctcttaccgaaccgactgtgccagcaggccaacctcgtaagat 473
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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RESULT 14
AC034198/c
LOCUS
DEFINITION
AC034198 Homo sapiens chromosome 3 clone RP11-767C1 map 3p, WORKING DRAFT
SEQUENCE, 25 unordered pieces.
AC034198
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 160214)
AUTHORS
Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H.,
Dong,W., Fan,H., Feng,X., Guan,Q., Gu,X., Guo,D., He,L., Hu,S.,
Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,G., Li,J., Li,L.,
Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W., Li,W., Li,Y.,
Luo,J., Niu,Y., Qi,Q., Qi,X., Song,S., Sun,M., Sun,W., Sun,Y.,
Tao,R., Wang,H., Wang,J., Wang,J., Wang,L., Wang,L., Wang,R.,
Wang,X., Wang,X., Wang,Y., Wu,D., Wu,Q., Xie,F., Xuan,Z., Xue,Y.,
Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G., Zhang,H., Zhang,H.,
Zhang,L., Zhang,M., Zhang,X., Zhang,X., Zhang,Y., Zhang,Y.,
Zhang,Z., Zhu,B., Yu,J. and Yang,H.
Unpublished
Chromosome 3p genomic sequence
TITLE
JOURNAL
REFERENCE
2 (bases 1 to 160214)
AUTHORS
Kang,N., Hu,S., Dong,W., Wang,J., Zhang,Y., Zhang,H., Liu,B.,
Bao,W., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y., Niu,Y.,
Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H., Liu,Y.,
Li,G., Li,C., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L., Guo,D.,
Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L., Feng,X., Yu,J.
and Yang,H.
Direct Submission
Submitted (05-APR-2000) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
COMMENT
On Sep 19, 2000 this sequence version replaced gi:8101278.
-----Genome Center
Center:Beijing Center
```



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* 138441 138540: gap of unknown length
* 138541 160214: Contig of 21674 bp in length.
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        1172..2254
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        2355..3851
            /note="assembly_name:Contig12"
        3952..5295
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        5396..6465
            /note="assembly_name:Contig14"
        6566..7857
            /note="assembly_name:Contig15"
        7958..9194
            /note="assembly_name:Contig16"
        9295..11038
            /note="assembly_name:Contig17"
        11139..14420
            /note="assembly_name:Contig18"
        14521..17864
            /note="assembly_name:Contig19"
        17965..21270
            /note="assembly_name:Contig20"
        21371..25050
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        clone_end:T7
            vector_side:right
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        42248..49752
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            /note="assembly_name:Contig28"
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        72621..83538
            /note="assembly_name:Contig30"
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        95314..107621
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            /note="assembly_name:Contig33"
        120612..138440
            /note="assembly_name:Contig34"
        138541..160214
            /note="assembly_name:Contig35"
BASE COUNT  40339 a 38297 c 38619 g 40533 t 2426 others
ORIGIN
Query Match          3.4%; Score 43.6; DB 54; Length
Best Local Similarity 48.4%; Pred. No. 0.74; Indels
Matches 121; Conservative 0; Mismatches 129; Indels
Oy 637 tacaacgctctgagcttgcgtgtcttgacagacctcagctccacgaata

```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 03:55:46 ; Search time 553.05 Seconds

(without alignments)
861.976 Million cell updates/sec

Title: US-09-380-276a-1

Perfect score: 1269

Sequence: 1 atgctttaaagtact.....ggcagcgactgggttcctg 1269

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_36:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1269	100.0	1496	19 V33362	Nucleotide sequenc
2	1267.4	99.9	1502	20 X08689	Novel nucleotide s
3	1256.2	99.0	1489	20 X23415	Human hAPO4-alpha
4	1244.8	98.1	1704	19 V33361	Nucleotide sequenc
5	1240	97.7	2185	20 X24978	Human TRAIN-R cDNA
6	835.6	65.8	987	20 X59346	Human NTR-5 cDNA
7	729.2	57.5	1678	20 X23413	Mouse hAPO4-alpha
8	449	35.4	886	20 X23414	Mouse hAPO4-alpha
9	449	35.4	942	20 X24977	Mouse TRAIN-R (lon
10	449	35.4	981	20 X87394	Mouse STRIFE1 (Tan
11	435.4	34.3	893	20 X84622	Human TNFR superfa
12	362.6	28.6	538	20 X59345	Mouse NTR-5 cDNA

13	361.6	28.5	371	19 V11422	Human secreted pro
14	314	24.7	591	20 X23417	Mouse hAPO4-gamma
15	314	24.7	599	20 X24976	Mouse TRAIN-R (sho
16	314	24.7	623	20 X84623	Mouse TNFR superfa
17	314	24.7	636	21 X92408	cDNA encoding murI
18	314	24.7	655	20 X87395	Mouse STRIFE2 (Tan
19	154.8	12.2	932	21 X2411	cDNA encoding huma
20	121.8	9.6	1133	20 X23416	Rat hAPO4-alpha DN
21	90.4	7.1	791	20 X24979	Clone GJ156 encodi
22	87.4	6.9	181	19 V11423	Human secreted pro
23	87.4	6.9	201	20 V86655	EST clone AX92. H
24	82	6.5	396	20 X23418	Mouse hAPO4-beta D
25	81.2	6.4	546	21 X2410	cDNA encoding huma
26	77.8	6.1	474	21 X92409	cDNA encoding huma
27	44	3.5	10732	21 A10594	Gene encoding a su
28	37.4	2.9	1290	20 X23121	Human TANGO 129 (T
29	37.4	2.9	2570	20 X23120	Human TANGO 129 (T
30	37.4	2.9	2703	21 D00061	Human tumour necro
31	36.4	2.9	1602	15 Q72217	Human adrenergic r
32	36.4	2.9	1978	15 Q72212	Truncated human al
33	36.4	2.9	1987	16 T11624	Human truncated al
34	36.4	2.9	1997	16 T11600	Human alpha-1C adr
35	36.4	2.9	1998	15 Q72213	Human alpha-1C adr
36	36.4	2.9	2004	16 T11599	Human alpha-1C adr
37	36.4	2.9	2005	15 Q72211	Human alpha-1C adr
38	36.2	2.9	330	21 A15982	Human protein clon
39	36.2	2.9	659	21 A15992	Human neurotransmi
40	36.2	2.9	2486	17 T09866	Human methyltransfer
41	36	2.8	2067	20 V99092	DNA methyltransfer
42	36	2.8	19440	20 V99129	Streptomyces hygro
43	35.6	2.8	1150	20 Z06928	Human cytoskeletal
44	35.2	2.8	1050	21 Z58975	Fragment 41-3 of t
45	35	2.8	326	11 Q05546	

ALIGNMENTS

RESULT 1

V33362

ID V33362 standard; cDNA to mRNA; 1496 BP.

XX AC V33362;

DT 02-DEC-1998 (first entry)

XX Nucleotide sequence of human beta-OAF065.

XX Human; beta-OAF065; stroma cell; antibody; inflammatory; cytokine-mediated disease; rheumatism; ulcerative colitis; ss.

KW Homo sapiens.

OS

XX Key Location/Qualifiers

FT CDS 45..1316

FT /*tag= a

FT /*product= "human beta-OAF065 protein"

FT sig_peptide 45..119

FT /*tag= b

FT mat_peptide 120..1313

FT /*tag= c

FT /transl_except= (pos:711..713, aa= Pro)

FT /transl_except= (pos:714..716, aa= Arg)

XX WO9838304-A1.

XX 03-SEP-1998.

XX 26-FEB-1998; 98WO-JP00799.

XX 27-FEB-1997; 97JP-0043143.

XX (ONOY) ONO PHARM CO LTD.

XX
PI Fukushima D, Konishi M, Tada H;
XX WPI: 1998-481205/41.
DR P-PSDB; W70387.
XX
PT Membrane polypeptide expressed by human stroma cells, and antibodies
PT recognising it - for treatment of inflammatory and other
PT cytokine-mediated diseases.
XX
PS Disclosure; Pages 40-41; 54pp; Japanese.
XX
CC This is the nucleotide sequence of the human beta-OAF065, used in
CC the method of the invention. The process involves the use of peptides
CC expressed by stroma cells, and its antibodies are used for in the
CC prevention and treatment of inflammatory and other cytokine-mediated
CC diseases such as rheumatism, ulcerative colitis.
XX
SQ Sequence 1496 BP; 388 A; 360 C; 372 G; 376 T; 0 other;

Query Match 100.0%; Score 1269; DB 19; Length 1496;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggctttaaaagtgtctactagacaagagaaaaacgtttttcactcttttagtattacta 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
45 atggctttaaaagtgtctactagacaagagaaaaacgtttttcactcttttagtattacta 104
QY 61 ggcattttgcatgtaagtgaactgttgaaacaggagactgtagacagcaagaattcagg 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
105 ggcattttgcatgtaagtgaactgttgaaacaggagactgtagacagcaagaattcagg 164
QY 121 gatcgtctgaaacgtgttccctgcaaccagtggtggccaggcagtgagttgtctaaag 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
165 gatcgtctgaaacgtgttccctgcaaccagtggtggccaggcagtgagttgtctaaag 224
QY 181 gaatgtgcttcggtatggggagtgatgcacagtgtgtgacgtgcccgtgcacaggttc 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
225 gaatgtgcttcggtatggggagtgatgcacagtgtgtgacgtgcccgtgcacaggttc 284
QY 241 aaggaggactggggcttccagaaatgcaagccctgtctggaactgcgagtggtgaaccgc 300
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285 aaggaggactggggcttccagaaatgcaagccctgtctggaactgcgagtggtgaaccgc 344
QY 301 ttccagaagcgaattgttcagccaccagtgatgccatctgcgggactgttgccaggga 360
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QY 361 ttatataggagacgaactgtcggtttcagagacatggagtgtgtgccttgtggagac 420
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405 ttatataggagacgaactgtcggtttcagagacatggagtgtgtgccttgtggagac 464
QY 421 cctctctctcttacaagccgactgtgccagcaagtgcaacctcgtgaagatcgcgctcc 480
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QY 481 acggctccagccagcagcagcagcgtgtgctgcccgttatctgcagcgtctggccacc 540
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525 acggctccagcagcagcagcagcgtgtgctgcccgttatctgcagcgtctggccacc 584
QY 541 gtctgtggtgcccgtgtcattcctctgtgtctatctattgttaagagacagtttatggagaag 600
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585 gtctgtggtgcccgtgtcattcctctgtgtctatctattgttaagagacagtttatggagaag 644
QY 601 aaaccagctggtctctgoggttcaagggacattcagtaaacggctctctgagctgctgctgt 660
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
645 aaaccagctggtctctgoggttcaagggacattcagtaaacggctctctgagctgctgctgt 704
QY 661 ctgtgacagacctcagctccacgaatgcccacagagctgctgcccagtcgcccgctgac 720
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
705 ctgtgacagacctcagctccacgaatgcccacagagctgctgcccagtcgcccgctgac 764

QY 721 tcagtgcagacctgcggccggtgcgcttgcctccatgcctccatgcctgcctgcctgcctgc 780
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825 agccccaaccccgagactcttgggtgtgggtgcattctgcagccagctcttcaggcaaga 884
QY 841 aacgcaggcccgagccgggagatggtgcgagactttcttggatccctccacgagtcacatc 900
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885 aacgcaggcccgagccgggagatggtgcgagactttcttggatccctccacgagtcacatc 944
QY 901 tggggcaggttttcagatgcctgcctctctgatgcagaatcccatgggtgtgagacaacatc 960
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1005 tcttttggactcttctatcctgaactcactgcgagagacattcattctctcattccacagaa 1064
QY 1021 ctggaagctcaacgtcttttgattcacaatagcagtcagaatttgggtggggtgtt 1080
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1065 ctggaagctcaacgtcttttgattcacaatagcagtcagaatttgggtggggtgtt 1124
QY 1081 ccagtcagctctctctctgaaactttacagcagctactgatttctatagatataacaac 1140
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1125 ccagtcagctctctctgaaactttacagcagctactgatttctatagatataacaac 1184
QY 1141 acactggtagaatcagcatcaactcaggatgcactaactatgagaagccagctagatcag 1200
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1185 acactggtagaatcagcatcaactcaggatgcactaactatgagaagccagctagatcag 1244
QY 1201 gaagtggtgcctatccaccagccactcagacgtccctccagtaagcagcagctg 1260
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1245 gaagtggtgcctatccaccagccactcagacgtccctccagtaagcagcagctg 1304
QY 1261 ggttcctcg 1269
Db ||||||||
1305 ggttcctcg 1313

RESULT 2
X08689
ID X08689 standard; cDNA; 1502 BP.
XX
AC X08689;
XX
XX 27-SEP-1999 (first entry)
XX
DE Novel nucleotide sequence encoding new protein (Clone AX92_3).
XX
XX Polynucleotide; protein; nutrition; cytokine; cell proliferation;
KW cell differentiation; immunostimulation; immunosuppression;
KW haematopoiesis regulation; tissue growth; activin; inhibin;
KW chemotaxis; chemokinesis; haemostasis; thrombolysis; receptor;
KW ligand; anti-inflammatory; tumour suppression; gene therapy; ds.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
CDS 51..1322
FT /*tag= a
FT /product= "Novel protein"
XX
XX WO920644-A1.
XX
PD 29-APR-1999.
XX
XX 16-OCT-1998; 98WO-US22034.
XX
PR 18-OCT-1997; 97US-0955557.
XX
XX (GEMY) GENETICS INST INC.

XX Agostino MJ, Bowman MR, Evans C, Jacobs K, Lavallie ER;
PI McCoy JM, Merberg D, Racie LA, Spaulding V, Treacy M;
XX
DR WPI: 1999-288272/24.
DR P-PSDB: W85724.
XX
XX New polynucleotides encoding secreted human proteins
PS
PS Claim 32; Page 116; 136pp; English.
XX
XX The new human secreted proteins are encoded by polynucleotides
CC obtained from human placenta, adult testes, fetal kidney, fetal
CC brain, adult brain, adult brain and adult blood cDNA libraries.
CC The polynucleotides and proteins are predicted to have biological
CC activities which would make them suitable for treating, preventing or
CC ameliorating medical conditions in humans and animals. Suggested
CC activities include nutritional activity, cytokine and cell
CC proliferation/differentiation activity, immune stimulating (e.g. as
CC vaccines) or suppressing activity, haematopoiesis regulating
CC activity, tissue growth activity, activin/inhibin activity,
CC chemotactic/chemokinetic activity, haemostatic and thrombolytic
CC activity, receptor/ligand activity, anti-inflammatory activity,
CC adherin/tumour invasion suppressor activity, and tumour inhibition
CC activity. The polynucleotides are also stated to be useful for gene
CC therapy. The sequences are identified by a secretory leader
CC sequence motif in the polynucleotide and it is thought that the
CC encoded proteins have biological activity by virtue of their secreted
CC nature. This clone was designated AX92_3. A probe for this clone is
CC described in X08704.
XX
XX Sequence 1502 BP; 388 A; 362 C; 375 G; 377 T; 0 other;
SQ

Query Match
Best Local Similarity 99.9%; Score 1267.4; DB 20; Length 1502;
Matches 1268; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 atgcttttaaagtctactagaacagagaaaacgtttttcactcttttagtattacta 60
Db
Qy 61 ggctatttgcattgataaagtacttgaacagagagacttagacagcaagaattcagg 120
Db
Qy 111 ggctatttgcattgataaagtacttgaacagagagacttagacagcaagaattcagg 170
Qy 121 gatcgtctgaaactgttctccctgcacacagtgatggccagcgatgagttgtctaa 180
Db 171 gatcgtctgaaactgttctccctgcacacagtgatggccagcgatgagttgtctaa 230
Qy 181 gaatgtgcttcggctatgggagagatgcacagtgatgacgtgcggtgcacaggttc 240
Db 231 gaatgtgcttcggctatgggagagatgcacagtgatgacgtgcggtgcacaggttc 290
Qy 241 aagagagactgggcttcagaaaatgaagccctgtctggactgcggtgcacagcgc 300
Db 291 aagagagactgggcttcagaaaatgaagccctgtctggactgcggtgcacagcgc 350
Qy 301 ttccagaaggcaaatgttccagccaccagtgcacatctgcgggagctgcttcaggga 360
Db 351 ttccagaaggcaaatgttccagccaccagtgcacatctgcgggagctgcttcaggga 410
Qy 361 tttatagaagacgaaactgtcgttttcaagacatggagtgctgcttggtagac 420
Db 411 tttatagaagacgaaactgtcgttttcaagacatggagtgctgcttggtagac 470
Qy 421 cctctcctcttaccagccgactgtgccagcaagggtcaacctcgtgaagatcgctcc 480
Db 471 cctctcctcttaccagccgactgtgccagcaagggtcaacctcgtgaagatcgctcc 530
Qy 481 acgggctccagcccgagacacggcgctggctgcgttatctgcagcgccttgccacc 540
Db 531 acgggctccagcccgagacacggcgctggctgcgttatctgcagcgccttgccacc 590

Qy 541 gtccctgtggccctgtcctcactcctgtgtcactcattgttaagagacagctttatgagaag 600
Db 591 gtccctgtggccctgtcctcactcctgtgtcactcattgttaagagacagctttatgagaag 650
Qy 601 aaacccagctggtctctgcgggtcagagacattcagtaacaacggtctctgactgctgtg 660
Db 651 aaacccagctggtctctgcgggtcagagacattcagtaacaacggtctctgactgctgtg 710
Qy 661 cttgacagactcagctccacgaatatgcccacagagcctgtcctcagtgccgctgac 720
Db 711 cttgacagactcagctccacgaatatgcccacagagcctgtcctcagtgccgctgac 770
Qy 721 tcagtgcagactcgcggccggtgcgtgtgctccatccatgctgtgagagagcctgcg 780
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Qy 841 aacgcagcccgagccgggagatggtgccgacttcttcgactcctcagcagcagcagcagc 900
Db 891 aacgcagcccgagccgggagatggtgccgacttcttcgactcctcagcagcagcagcagc 950
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Db 1251 gagagtggtcgtatcattccacccagccactcagacgttccctccaggttaaggcagcagctg 1310
Qy 1261 ggttccctg 1269
Db 1311 ggttccctg 1319

RESULT 3

X23415
ID X23415 standard; DNA; 1489 BP.

XX X23415;

XX X23415;

DT 18-JUN-1999 (first entry)

XX Human hAPO4-alpha DNA.

XX Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW developmental abnormality; gestational abnormality; prostate cancer;
KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW apoptosis; human; APO4-alpha; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT	CDS	65..1336	
FT	FT	/tag= a	
FT	FT	/product= "hAPO4-alpha"	
XX	PN	WO9911791-A2.	
XX	XX		
PD	PD	11-MAR-1999.	
XX	XX		
PF	PF	04-SEP-1998; 98WO-US18393.	
XX	XX		
PR	PR	05-SEP-1997; 97US-0924634.	
XX	XX		
PA	PA	(UNIW) UNIV WASHINGTON.	
XX	XX		
PI	PI	Chaudhary PW;	
XX	XX		
DR	DR	WPI; 1999-205191/17.	
XX	XX	P-PSDB; W93581.	
PT	PT	New Tumor Necrosis Factor family receptor polypeptides and ligands -	
PT	PT	useful for diagnosis and treatment of prostate cancer and	
PT	PT	developmental or gestational abnormalities	
XX	XX		
PS	PS	Example IV; Fig 7C; 156pp; English.	
XX	XX		
CC	CC	This invention describes isolated Tumor Necrosis Factor (TNF) family	
CC	CC	receptor polypeptides; APO4, APO6, APO8 and APO9 or their active	
CC	CC	fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or	
CC	CC	their active fragments. APO4 is useful for diagnosing prostate cancer	
CC	CC	by determining levels of APO4 in an individual. Prostate cancer can also	
CC	CC	be treated using APO4 selective binding agents linked to a therapeutic	
CC	CC	moiety. APO4 polypeptides are also useful for identifying selective	
CC	CC	binding agents, useful in diagnosis/treatment of disease by binding of	
CC	CC	agents to the polypeptide/active fragment which is extracellular, or	
CC	CC	expressed on the cell surface. The binding is preferably performed in	
CC	CC	vivo. APO4 polypeptides/ active fragments are also useful for screening	
CC	CC	for agonists and antagonists by binding and observing the change in APO4	
CC	CC	activity. Effective pharmacological agents useful in diagnosis or	
CC	CC	treatment of disease are also identified using APO4 polypeptides/active	
CC	CC	fragments and APO4 signal transducer molecules that specifically interact	
CC	CC	with a cytoplasmic domain of APO4 and detecting a change in level of APO4	
CC	CC	activity. The method is performed in vivo or in vitro. APO polypeptides	
CC	CC	are all useful as immunogens for preparing antibodies. APO4 is also	
CC	CC	useful for diagnosis/treatment of developmental or gestational	
CC	CC	abnormalities. APO8 was transfected to human breast carcinoma cell line	
CC	CC	MCF-7, and induced apoptosis.	
XX	XX		
SQ	SQ	Sequence 1489 BP; 361 A; 366 C; 380 G; 382 T; 0 other;	
Query Match 99.0%; Score 1256.2; DB 20; Length 1489;			
Best Local Similarity 99.4%; Pred. No. 0;			
Matches 1261; Conservative 0; Mismatches 8; Indels 0; Gaps 0;			
QY	QY	1 atggccttaaaagtgtactagacaagagaaaacgtttttcactcttttagtattacta 60	
DB	DB		
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QY	QY	125 ggtattttgtcattgaagtgaactgtgtgaaacaggagactgtagacagcaagaattcagg 184	
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DB	DB		
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QY	QY	181 gaatgtggcttcggctatggggaggatgcacagtggtgtgacgtgcggctgcacaggttc 240	
DB	DB		
QY	QY	245 gaatgtggcttcggctatggggaggatgcacagtggtgtgacgtgcggctgcacaggttc 304	
DB	DB		
QY	QY	241 aagagagactggggctccagaataacagccctgtctgagactgcagtcggtgaaccgc 300	
DB	DB		
QY	QY	305 aagagagactggggctccagaataacagccctgtctgagactgcagtcggtgaaccgc 364	
DB	DB		

RESULT 4

V33361

ID V33361 standard; cDNA to mRNA; 1704 BP.

X23414
ID X23414 standard; DNA; 886 BP.
XX
AC X23414;
XX
DT 18-JUN-1999 (first entry)
XX
DE Mouse mAPO4-alpha (short) DNA.
XX
KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
KW developmental abnormality; gestational abnormality; prostate cancer;
KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW apoptosis; mouse; mAPO4-alpha; ss.
XX
OS Mus sp.
XX
XX
FH Key Location/Qualifiers
FT CDS 72..716
FT /*tag= a
FT /product= "mAPO4-alpha short"
XX
PN WO9911791-A2.
XX
PD 11-MAR-1999.
XX
PF 04-SEP-1998; 98WO-US18393.
XX
PR 05-SEP-1997; 97US-0924634.
XX
XX (UNIW) UNIV WASHINGTON.
XX
XX Chaudhary PM;
XX
XX WPI: 1999-205191/17.
XX P-PSDB; W93580.
XX
XX New Tumor Necrosis Factor family receptor polypeptides and ligands -
XX useful for diagnosis and treatment of prostate cancer and
XX developmental or gestational abnormalities
XX
XX Example IV; Fig 7B; 156pp; English.
XX
XX This invention describes isolated Tumor Necrosis Factor (TNF) family
XX receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
XX fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
XX their active fragments. APO4 is useful for diagnosing prostate cancer
XX by determining levels of APO4 in an individual. Prostate cancer can also
XX be treated using APO4 selective binding agents linked to a therapeutic
XX moiety. APO4 polypeptides are also useful for identifying selective
XX binding agents, useful in diagnosis/treatment of disease by binding of
XX agents to the polypeptide/active fragment which is extracellular, or
XX expressed on the cell surface. The binding is preferably performed in
XX vivo. APO4 polypeptides/ active fragments are also useful for screening
XX for agonists and antagonists by binding and observing the change in APO4
XX activity. Effective pharmacological agents useful in diagnosis or
XX treatment of disease are also identified using APO4 polypeptides/active
XX fragments and APO4 signal transducer molecules that specifically interact
XX with a cytoplasmic domain of APO4 and detecting a change in level of APO4
XX activity. The method is performed in vivo or in vitro. APO polypeptides
XX are all useful as immunogens for preparing antibodies. APO4 is also
XX useful for diagnosis/treatment of developmental or gestational
XX abnormalities. APO8 was transfected to human breast carcinoma cell line
XX MCF-7, and induced apoptosis.
XX
XX Sequence 886 BP; 204 A; 245 C; 247 G; 190 T; 0 other;
XX
XX
XX Query Match 35.4%; Score 449; DB 20; Length 886;
XX Best Local Similarity 82.4%; Pred. No. 4.9e-128;
XX Matches 515; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
XX
XX 1 atgctttaaagtgtactagaacaagaaacgtttttcactctttttatttacta 60

Db 72 atggcaactcaaggtcctacctctacacagagcggtgtctcttcgtgccattctcttcta 131
Qy 61 ggctatttgtcatgtataagtgacttgtgaacacagagagacttagacacagaatactcagg 120
Db 132 ctccactggcatgtataagtgactgtgcgaaccggagattgcaggcagcagaatactcaag 191
Qy 121 gatcggtctgaaactgtgtccctgcacacagtgatggccagcgcatgagttgtcttaag 180
Db 192 gatgatctgaaactgtgtcctctgcaaacagtcggacacctggcatgagttgtcccaag 251
Qy 181 gaatgtgcttcggctatgggagagatgcacagtgatgtgacgtgcggctgcacaggttc 240
Db 252 gaatgtgcttcggctatgggagagatgcacagtgatgtgacgtgcggctgcacaggttc 311
Qy 241 aaggagagactgggctctccagaaatgcagccctgtctggactgcgagtggtgaaccgc 300
Db 312 aaggagagactgggctctccagaaatgcagccctgtctggactgcgagtggtgaaccgc 371
Qy 301 ttccagaagggcaaatgttcagccaccagtgatgcacatcgcgggagactgcttgcaggga 360
Db 372 ttccagaagggcaaatgttcagccaccagtgatgcacatcgcgggagactgcttgcaggga 431
Qy 361 ttttataggagaagaaactgttcagcccttcaagacatggagtggtgcttgcaggagac 420
Db 432 tttaccgggaagaccactgtgtgttttcaagacatggagtggtgcttgcaggagac 491
Qy 421 cctcctcctcttacgaaccgactgtgccacagcaggtcaacctgtgaagatcgctcc 480
Db 492 ccactcctcctacgaaccacactgtaccacagcaggtgaacctgtgaagatcctccc 551
Qy 481 acggcctccagccacgggacacggcgctgcctcgttatctgcagcgctctgcccacc 540
Db 552 accgtctccagccctcgggacacggcgctgcctcgttatctgcagcgctctgcccacc 611
Qy 541 gtctgtgctgcccgtcctcctctgtgtcattctatttgaagagacagtttatggagaag 600
Db 612 gtctgtgctgcccgtcctcctctgtgtcattctactgcaagagcaggttcattggagaag 671
Qy 601 aaacccagctgtctctgcgacac 625
Db 672 aaacccagctgttaagctcccatccc 696
RESULT 9
X24977
ID X24977 standard; cDNA; 942 BP.
XX
AC X24977;
XX
DT 05-JUL-1999 (first entry)
XX
DE Mouse TRAIN-R (long form) cDNA.
XX
KW TRAIN-R; receptor; mouse; tumour necrosis factor receptor;
KW agonist; antagonist; cancer; immunological disease; therapy;
XX cytostatic; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 101..745
FT /*tag= a
XX
PN WO9913078-A1.
XX
XX 18-MAR-1999.
XX
XX 11-SEP-1998; 98WO-US19030.
XX
XX 06-MAY-1998; 98US-0084422.
XX
XX 12-SEP-1997; 97US-0058631.
XX


```

ID  V11422 standard; cDNA; 371 BP.
XX  V11422;
AC  V11422;
XX  23-JUL-1998 (first entry)
DT  Human secreted protein clone AX92_3 cDNA 5'-end.
DE  Secreted protein; prevention; treatment; gene therapy; ds.
XX  Homo sapiens.
XX  W09801554-A2.
XX  15-JAN-1998.
XX  07-JUL-1997; 97WO-US11876.
XX  09-JUL-1996; 96US-0677231.
XX  (GEMY ) GENETICS INST INC.
XX  Bowman M, Evans C, Jacobs K, LaVallie ER, McCoy JM;
PI  Werberg D, Racine LA, Spaulding V, Treacy M;
XX  WPI; 1998-110230/10.
XX  P-PSDB; W58844.
XX  Secreted proteins and polynucleotides encoding them - useful to
PT  prevent, treat and ameliorate medical conditions
XX  Claim 15; Page 57; 93pp; English.
XX  V11422-V11424 encode fragments of a novel secreted protein derived from
CC  clone AX92_3 which was isolated from a human adult testes cDNA library.
CC  The protein can be used to prevent, treat or ameliorate a medical
CC  condition, while the polynucleotides can be used for gene therapy.
XX  Sequence 371 BP; 83 A; 96 C; 107 G; 82 T; 3 other;

Query Match 28.5%; Score 361.6; DB 19; Length 371;
Best Local Similarity 98.1%; Pred. NO. 2.2e-101;
Matches 364; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 128 ctggaactgtgttccctgcacacagtggtggccaggcatggagtggtcttaaggaaatgtg 187
DB 1 ctggaactgtgttccctgcacacagtggtggccaggcatggagtggtcttaaggaaatgtg 60
OY 188 gcttcggctatgggagatgcacacagtggtgacgtgcgcgctgcacacaggttcaaggagg 247
DB 61 gcttcggctatgggagatgcacacagtggtgacgtgcgcgctgcacacaggttcaaggagg 120
OY 248 actgggggttcagaaatgcagccctgtctgactgcgcagtggtgacgcgttttcaga 307
DB 121 actgggggttcagaaatgcagccctgtctgactgcgcagtggtgacgcgttttcaga 180
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DB 181 aggcgaattgttcagccacagtgatgccatctgcgggactggttcgaggattttata 240
OY 368 ggaacagcaacttgcggcttcacagcatgagtggtgctgttgagacctctc 427
DB 241 ggaacacnaacttgcggcttcacacatgagtggtgctgttgagacctctc 300
OY 428 ctcttaagcaaccgactgtgcccagcaaggtcaacctgtaagatcggtccacggcct 487
DB 301 ctcttaagcaaccgactgtgcccagcaaggtcaacctgtaagatcggtccacggcct 360
OY 488 ccagccacgg 498
DB 361 ccagccacgg 371

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RESULT 14

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X23417
ID  X23417 standard; DNA; 591 BP.
XX  X23417;
AC  X23417;
XX  18-JUN-1999 (first entry)
DT  Mouse mAPO4-gamma DNA.
DE  Mouse mAPO4-gamma DNA.
XX  Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
XX  developmental abnormality; gestational abnormality; prostate cancer;
KW  APO6; APO8; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
KW  cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
KW  apoptosis; mouse; APO4-gamma; ss.
XX  Mus sp.
XX  Key Location/Qualifiers
XX  CDS 95..547
XX  FT /*tag= a
XX  FT /product= "mAPO4-gamma"
XX  W09911791-A2.
XX  11-MAR-1999.
XX  04-SEP-1998; 98WO-US18393.
XX  05-SEP-1997; 97US-0924634.
XX  (UNIW ) UNIV WASHINGTON.
XX  Chaudhary PM;
XX  WPI; 1999-205191/17.
XX  P-PSDB; W93583.
XX  New Tumor Necrosis Factor family receptor polypeptides and ligands -
XX  useful for diagnosis and treatment of prostate cancer and
XX  developmental or gestational abnormalities
XX  Disclosure; Fig 7E; 156pp; English.
XX  This invention describes isolated Tumor Necrosis Factor (TNF) family
XX  receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
XX  fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
XX  their active fragments. APO4 is useful for diagnosing prostate cancer
XX  by determining levels of APO4 in an individual. Prostate cancer can also
XX  be treated using APO4 selective binding agents linked to a therapeutic
XX  moiety. APO4 polypeptides are also useful for identifying selective
XX  binding agents, useful in diagnosis/treatment of disease by binding of
XX  agents to the polypeptide/active fragment which is extracellular, or
XX  expressed on the cell surface. The binding is preferably performed in
XX  vivo. APO4 polypeptides/ active fragments are also useful for screening
XX  for agonists and antagonists by binding and observing the change in APO4
XX  activity. Effective pharmacological agents useful in diagnosis or
XX  treatment of disease are also identified using APO4 polypeptides/active
XX  fragments and APO4 signal transducer molecules that specifically interact
XX  with a cytoplasmic domain of APO4 and detecting a change in level of APO4
XX  activity. The method is performed in vivo or in vitro. APO polypeptides
XX  are all useful as immunogens for preparing antibodies. APO4 is also
XX  useful for diagnosis/treatment of developmental or gestational cell line
XX  abnormalities. APO8 was transfected to human breast carcinoma cell line
XX  MCF-7, and induced apoptosis.
XX  Sequence 591 BP; 148 A; 145 C; 175 G; 123 T; 0 other;

Query Match 24.7%; Score 314; DB 20; Length 591;
Best Local Similarity 78.9%; Pred. NO. 1.2e-86;
Matches 374; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2001, 03:51:51 ; Search time 217.59 Seconds

(without alignments)

939,898 Million cell updates/sec

Title: US-09-380-276A-1

Perfect score: 1269

Sequence: 1 atggttttaaaagtctact.....ggcagcgactgggttccttg 1269

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 280836 seqs, 80580151 residues

Total number of hits satisfying chosen parameters: 561672

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36.4	2.9	1601	1 US-08-722-001-7	Sequence 7, Appli
2	36.4	2.9	1987	1 US-08-722-001-26	Sequence 26, Appl
3	36.4	2.9	1997	1 US-08-722-001-27	Sequence 27, Appl
4	36.4	2.9	2004	1 US-08-722-001-11	Sequence 11, Appl
5	36.2	2.9	2485	1 US-08-424-424B-1	Sequence 1, Appli
6	36.2	2.9	2486	4 PCT-US94-05363A-1	Sequence 1, Appli
7	34.8	2.7	1639	1 US-08-334-698-5	Sequence 5, Appli
8	34.8	2.7	1639	1 US-08-228-932-5	Sequence 5, Appli
9	34.8	2.7	1639	1 US-08-468-939-5	Sequence 5, Appli
10	34.8	2.7	1639	2 US-08-406-855A-5	Sequence 5, Appli
11	34.8	2.7	1639	2 US-08-722-190-5	Sequence 5, Appli
12	34.8	2.7	1639	3 US-08-244-354-5	Sequence 5, Appli
13	34.8	2.7	1639	3 US-09-206-899-5	Sequence 5, Appli
14	34.8	2.7	1639	4 PCT-US95-04203-5	Sequence 5, Appli
15	34.6	2.7	5962	5 5386025-5	Patent No. 5386025
16	34.6	2.7	7218	1 US-08-232-463-14	Sequence 14, Appli
17	33.6	2.6	800	2 US-08-416-603-11	Sequence 11, Appli
18	33.4	2.6	4360	1 US-08-470-350B-1	Sequence 1, Appli
19	33	2.6	9472	1 US-08-325-547-9	Sequence 9, Appli
20	32.8	2.6	2230	1 US-08-200-512-1	Sequence 1, Appli
21	32.6	2.6	1593	2 US-08-524-828-2	Sequence 2, Appli
22	32.6	2.6	1593	2 US-08-975-114A-2	Sequence 2, Appli
23	32.6	2.6	1593	3 US-08-849-281A-2	Sequence 2, Appli
24	32.6	2.6	2247	2 US-08-524-828-1	Sequence 1, Appli
25	32.6	2.6	2247	2 US-08-975-114A-1	Sequence 1, Appli
26	32.6	2.6	3891	1 US-08-480-604A-27	Sequence 27, Appl
27	32.6	2.6	3891	2 US-08-405-496A-27	Sequence 27, Appl
28	32.4	2.6	1167	1 US-07-960-985-1	Sequence 1, Appli

29 32.4 2.6 1167 2 US-08-496-671-1 Sequence 1, Appli
30 32.4 2.6 1690 2 US-08-461-812-3 Sequence 3, Appli
31 32.4 2.6 3083 2 US-08-480-994-36 Sequence 36, Appli
32 32.4 2.6 3083 2 US-08-616-844-36 Sequence 36, Appli
33 32.4 2.6 3083 2 US-08-599-654-36 Sequence 36, Appli
34 32.4 2.6 3083 2 US-08-485-573-36 Sequence 36, Appli
35 32.4 2.6 3083 3 US-08-944-868A-36 Sequence 36, Appli
36 32.4 2.6 3083 3 US-08-944-423A-36 Sequence 36, Appli
37 32.4 2.6 3083 3 US-08-925-743-36 Sequence 36, Appli
38 32.4 2.6 3083 3 US-08-944-496-36 Sequence 36, Appli
39 32.4 2.6 3084 3 US-08-826-246-11 Sequence 11, Appli
40 32.4 2.6 3084 3 US-08-944-495-11 Sequence 11, Appli
41 32.4 2.6 3084 3 US-09-126-640-6 Sequence 11, Appli
42 32.4 2.6 28804 3 US-08-592-874-1 Sequence 1, Appli
43 32.4 2.6 28804 3 US-09-096-942-2 Sequence 2, Appli
44 32.4 2.6 28804 3 US-09-096-867-2 Sequence 2, Appli
45 32.2 2.5 953 1 US-08-197-793-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-722-001-7
; Sequence 7, Application US/08722001
; Patent No. 5760054
; GENERAL INFORMATION:
; APPLICANT: Thompson, Wayne J.
; APPLICANT: Huff, Joel R.
; APPLICANT: Nerenberg, Jennie B.
; APPLICANT: Lee, Hee-Yoon
; APPLICANT: Bell, Ian M.
; TITLE OF INVENTION: ALPHAIIC ADRENERGIC RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,001
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/229,276
; FILING DATE: 14-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Appollina, Mary A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19169Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-722-001-7

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Query Match      2.9%; Score 36.4; DB 1; Length 1601;
Best Local Similarity 52.7%; Pred. No. 0.18;
Matches 79; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 474 cgcgtccacggcctccagccacgggagacacggcgctgtgctgtatctgacgcgtct 533
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1107 CGAGGAGGAGACCATCTGCCAGATCAACAGGAGCGCGGCTACGTCTCTTCGGCTCT 1166

QY 534 ggcacgcctctgctgctcctctcctctgtgtcatctattgtaagagacagtttat 593
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1167 GGCTCTCTTACTGCTCTGCCCATCATCTGGTGCATCTACTGCGCGCTCTACGTGGT 1226

QY 594 ggagaagaacccagctgtctctgcggtc 623
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Db 1227 GGCAAGAGGAGAGCGCGGCTCAAGTC 1256

RESULT 2
US-08-722-001-26
; Sequence 26, Application US/08722001
; Patent No. 5760054
; GENERAL INFORMATION:
; APPLICANT: Thompson, Wayne J.
; APPLICANT: Huff, Joel R.
; APPLICANT: Nerenberg, Jennie B.
; APPLICANT: Lee, Hee-Yoon
; APPLICANT: Bell, Ian M.
; TITLE OF INVENTION: ALPHAIC ADRENERGIC RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,001
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/229,276
; FILING DATE: 14-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Appollina, Mary A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19169Y
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1987 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; US-08-722-001-26

Query Match      2.9%; Score 36.4; DB 1; Length 1987;
Best Local Similarity 52.7%; Pred. No. 0.21;
Matches 79; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 474 cgcgtccacggcctccagccacgggagacacggcgctgtgctgtatctgacgcgtct 533
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Db 1112 CGAGGAGGAGACCATCTGCCAGATCAACAGGAGCGCGGCTACGTCTCTTCGGCTCT 1171

QY 534 ggcacgcctctgctgctcctctcctctgtgtcatctattgtaagagacagtttat 593
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Db 1172 GGGCTCTCTTACTGCTCTGCCCATCATCTGGTGCATCTACTGCGCGCTCTACGTGGT 1231

QY 594 ggagaagaacccagctgtctctgcggtc 623
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Db 1232 GGCAAGAGGAGAGCGCGGCTCAAGTC 1261

RESULT 3
US-08-722-001-27
; Sequence 27, Application US/08722001
; Patent No. 5760054
; GENERAL INFORMATION:
; APPLICANT: Thompson, Wayne J.
; APPLICANT: Huff, Joel R.
; APPLICANT: Nerenberg, Jennie B.
; APPLICANT: Lee, Hee-Yoon
; APPLICANT: Bell, Ian M.
; TITLE OF INVENTION: ALPHAIC ADRENERGIC RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,001
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/229,276
; FILING DATE: 14-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Appollina, Mary A.
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19169Y
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1997 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; HYPOTHEtical: NO
; ANTI-SENSE: NO
; US-08-722-001-27

Query Match      2.9%; Score 36.4; DB 1; Length 1997;
Best Local Similarity 52.7%; Pred. No. 0.21;
Matches 79; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 474 cgcgtccacggcctccagccacgggagacacggcgctgtgctgtatctgacgcgtct 533
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1106 CGAGGAGGAGACCATCTGCCAGATCAACAGGAGCGCGGCTACGTCTCTTCGGCTCT 1165

QY 534 ggcacgcctctgctgctcctctcctctgtgtcatctattgtaagagacagtttat 593
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

: APPLICANT: LI, ET AL.
 : TITLE OF INVENTION: Neurotransmitter Transporter
 : NUMBER OF SEQUENCES: 2
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN.
 :

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41378-B/JPW/TEP
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: (212) 422523 COOP UI
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1639 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 126..1523
OTHER INFORMATION:
US-08-228-932-5

Query Match 2.7%; Score 34.8; DB 1; Length 1639;
Best Local Similarity 52.0%; Pred. No. 0.59;
Matches 78; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 474 cgcgtccacggcctccagccacggcggacacggcgtggtcgcttatctgcagcgctct 533
DB 635 CGAGGACGAGACCATGCGCAGATCAACGAGGAGCGGGCTACGTGCTCTTCTCAGCGCT 694

QY 534 gccaccgtcctgctggccctcctcctctgtgtcatctattgttaagagacagtttat 593
DB 695 GGGCTCCTTCTACCTGCCCTCTGGCCATCATCTGTCATGTACTGCCGCGCTACGTGCT 754

QY 594 ggagagaacacccagctgctctctcggtc 623
DB 755 GGCCAAAGAGGAGAGCGGGGCTCAAGTC 784

RESULT 9
US-08-468-939-5
Sequence 5, Application US/08468939
Patent No. 5714381
GENERAL INFORMATION:
APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,939
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41377-1B
TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1639 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 126..1523
OTHER INFORMATION:
US-08-468-939-5

Query Match 2.7%; Score 34.8; DB 1; Length 1639;
Best Local Similarity 52.0%; Pred. No. 0.59;
Matches 78; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 474 cgcgtccacggcctccagccacggcggacacggcgtggtcgcttatctgcagcgctct 533
DB 635 CGAGGACGAGACCATGCGCAGATCAACGAGGAGCGGGCTACGTGCTCTTCTCAGCGCT 694

QY 534 gccaccgtcctgctggccctcctcctctgtgtcatctattgttaagagacagtttat 593
DB 695 GGGCTCCTTCTACCTGCCCTCTGGCCATCATCTGTCATGTACTGCCGCGCTACGTGCT 754

QY 594 ggagagaacacccagctgctctctcggtc 623
DB 755 GGCCAAAGAGGAGAGCGGGGCTCAAGTC 784

RESULT 10
US-08-406-855A-5
Sequence 5, Application US/08406855A
Patent No. 5861309
GENERAL INFORMATION:
APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,855A
FILING DATE: 21-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KDB
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1639 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)

;
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 126..1523
; OTHER INFORMATION:
; US-08-406-855A-5

Query Match 2.7%; Score 34.8; DB 2; Length 1639;
Best Local Similarity 52.0%; Pred. No. 0.59; Mismatches 0; Indels 0; Gaps 0;
Matches 78; Conservative 0;
QY 474 cgcgtccacggcctccagccacgggacgagcgctggtcgtgctggtatctgcagcgctct 533
DB 635 CGAGGACGAGACCATCTGCCAGATCAACGAGGAGCGGGCTACGTGCTCTCTCAGCGCT 694
QY 534 ggcacgcgtcgtggtgcccctgcctcctctgtgctatctattgtaagagacagtttat 593
DB 695 GGGCTCCTTCTACTGCTCTGGCCATCATCCTGCTGCTACTGCGCGCTACGTGGT 754
QY 594 ggagaaagaaacccagctggtctctgcggtc 623
DB 755 GGCCAGAGGAGGAGCGGGCGCTCAAGTC 784

RESULT 11

US-08-722-190-5
; Sequence 5, Application US/08722190
; Patent No. 5990128
; GENERAL INFORMATION:
; APPLICANT: Charles Gluchowski, Carlos C. Forray, George
; APPLICANT: Chiu, Theresa A. Branchek, John M. Wetzel and Paul R. Hartig
; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
; TITLE OF INVENTION: TREAT BENIGN PROSTATIC HYPERPLASIA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,190
; FILING DATE: 4-APR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41878-D-PCT/JPW/AGL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1639 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 126..1523
; OTHER INFORMATION:
;

Query Match 2.7%; Score 34.8; DB 3; Length 1639;
Best Local Similarity 52.0%; Pred. No. 0.59; Mismatches 0; Indels 0; Gaps 0;
Matches 78; Conservative 0;

US-08-722-190-5

Query Match 2.7%; Score 34.8; DB 2; Length 1639;
Best Local Similarity 52.0%; Pred. No. 0.59; Mismatches 0; Indels 0; Gaps 0;
Matches 78; Conservative 0;
QY 474 cgcgtccacggcctccagccacgggacgagcgctggtcgtgctggtatctgcagcgctct 533
DB 635 CGAGGACGAGACCATCTGCCAGATCAACGAGGAGCGGGCTACGTGCTCTCTCAGCGCT 694
QY 534 ggcacgcgtcgtggtgcccctgcctcctctgtgctatctattgtaagagacagtttat 593
DB 695 GGGCTCCTTCTACTGCTCTGGCCATCATCCTGCTGCTACTGCGCGCTACGTGGT 754
QY 594 ggagaaagaaacccagctggtctctgcggtc 623
DB 755 GGCCAGAGGAGGAGCGGGCGCTCAAGTC 784

RESULT 12

US-08-244-354-5
; Sequence 5, Application US/08244354
; Patent No. 6015819
; GENERAL INFORMATION:
; APPLICANT: Charles Gluchowski, et al.
; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
; TITLE OF INVENTION: TREAT BENIGN PROSTATIC HYPERPLASIA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,354
; FILING DATE: April 1, 1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41878-D-PCT-US/JPW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1639 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 126..1523
; OTHER INFORMATION:
; US-08-244-354-5

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 16, 2001, 21:09:00 ; Search time 53.31 Seconds
(without alignments)
930.012 Million cell updates/sec

Title: US-09-380-276A-8

Perfect score: 2283

Sequence: 1 MALKVLEQEKTFLLVLL.....AIHPATQSLQVRQLGSL 423

Scoring table:

BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_15:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2274	99.6	423	4 Q9NS68	Q9ns68 homo sapien
2	2258	98.9	423	4 Q9NZV2	Q9nzv2 homo sapien
3	1559.5	68.3	416	11 Q9JUH6	Q9jih6 mus musculus
4	1557.5	68.2	416	11 Q9JUL3	Q9jil3 mus musculus
5	1472.5	64.5	348	11 Q9QXW7	Q9qxw7 mus musculus
6	977	42.8	214	11 Q9JHF1	Q9jhf1 mus musculus
7	725	31.8	150	11 Q9JLL2	Q9jll2 mus musculus
8	197	8.6	448	11 Q9RI87	Q9ri87 mus musculus
9	191	8.4	448	4 Q9UNE0	Q9une0 homo sapien
10	191	8.4	448	4 Q9UND9	Q9und9 homo sapien
11	170.5	7.5	387	13 Q9PVD4	Q9pvd4 xenopus lae
12	144.5	6.3	430	6 Q9N092	Q9n092 macaca fasc
13	142	6.2	417	11 Q9Z0W1	Q9z0w1 mus musculus
14	142	6.2	426	4 O14865	O14865 homo sapien
15	137.5	6.0	186	12 O72735	O72735 cowpox viru
16	136	6.0	625	11 O35305	O35305 mus musculus
17	134.5	5.9	3396	5 Q9VM55	Q9vm55 drosophila
18	134	5.9	186	12 Q9YP87	Q9yp87 cowpox viru
19	134	5.9	277	4 O14866	O14866 homo sapien

20	134	5.9	348	12	O57277	monkeypox v
21	134	5.9	348	12	O57103	monkeypox v
22	134	5.9	348	12	O57108	monkeypox v
23	133.5	5.8	350	12	O57123	cowpox viru
24	133	5.8	543	5	Q9VJU5	Q9vjus drosophila
25	133	5.8	620	5	Q9NKD8	Q9nkds drosophila
26	132.5	5.8	3680	5	Q9VR08	Q9vr08 drosophila
27	131.5	5.8	349	12	O57291	monkeypox v
28	131.5	5.8	349	12	O57099	monkeypox v
29	131.5	5.8	349	12	O57100	monkeypox v
30	131.5	5.8	349	12	O57101	monkeypox v
31	131.5	5.8	349	12	O57102	monkeypox v
32	130	5.7	186	12	Q9WJB4	Q9wjbs vaccinia vi
33	129.5	5.7	1254	13	Q9VHU2	Q9yhu2 brachydanio
34	128	5.6	347	12	O57115	cowpox viru
35	128	5.6	355	12	O85308	cowpox viru
36	128	5.6	401	13	Q9PRG7	Q9prg7 xenopus lae
37	127.5	5.6	349	12	O57111	variola vir
38	127	5.6	1114	11	Q9JKW7	Q9jkw7 mus musculus
39	127	5.6	1650	11	Q9QVT6	Q9qvt6 rattus sp.
40	127	5.6	1792	13	O57484	Q57484 gallus gall
41	127	5.6	1827	5	O20535	Q20535 caenorhabdi
42	126.5	5.5	380	4	O00280	O00280 homo sapien
43	126.5	5.5	1394	5	Q9VS89	Q9vs89 drosophila
44	126	5.5	349	12	O57305	cowpox viru
45	126	5.5	350	12	O57116	cowpox viru

ALIGNMENTS

RESULT 1

Q9NS68 PRELIMINARY; PRT; 423 AA.

AC Q9NS68;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE HTROY.

GN HTROY.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

[1]

RP SEQUENCE FROM N.A.

RA Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,

RA Senba E., Kitamura T.;

RT "TROY, a newly identified member of the tumor necrosis factor receptor

superfamily, exhibits a homology with edar and is expressed in

embryonic skin and hair follicles.";

J. Biol. Chem. 275:20742-20747(2000).

DR EMBL; AB040434; BAB03269.1; -

SQ SEQUENCE 423 AA; 46015 MW; B5891CEA9ED45361 CRC64;

Query Match 99.6%; Score 2274; DB 4; Length 423;

Best Local Similarity 99.3%; Pred. No. 5.6e-202;

Matches 420; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MALKVLEQEKTFLLVLLGLYLSCKVTCGTGDCRQEQFRDRSGNCVPCNCGPGMELSK 60

|||||

Db 1 MALKVLEQEKTFLLVLLGLYLSCKVTCGTGDCRQEQFRDRSGNCVPCNCGPGMELSK 60

|||||

Qy 61 ECGFGYGEDAQCVTCRLHFRFEDWGFKCKPCLDCAVVNRQKNCATSATSDAICGDLPG 120

|||||

Db 61 ECGFGYGEDAQCVTCRLHFRFEDWGFKCKPCLDCAVVNRQKNCATSATSDAICGDLPG 120

|||||

Qy 121 FYRKTGLVGFODMECVPCGDPDPPEPHCAKSNLVKLTASTASSPRDTALAIVICSALAT 180

|||||

Db 121 FYRKTGLVGFODMECVPCGDPDPPEPHCAKSNLVKLTASTASSPRDTALAIVICSALAT 180

|||||

Qy 181 VLLALLILCVIYCKRQFMKEKPSWSLRSQDIQYNGSELSCSLDRPOLHEYAHRAACQCRRD 240

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Db 181 VLLALLILCVYKROFMKKPSWLSRSQDIQYNGSELSCFDRPQLHEYAHRAACCCRRD 240
QY 241 SVOTCGPVRLLPSMCCCEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Db 241 SVOTCGPVRLLPSMCCCEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
QY 301 CGEFSDAWPLMQNPMGDDNISFCDSYPCLTGEDIHSLNPELESSTSLDSSODLVGGAV 360
Db 301 CGEFSDAWPLMQNPMGDDNISFCDSYPCLTGEDIHSLNPELESSTSLDSSODLVGGAV 360
QY 361 PVOSHENFTAAATDLRYNNLTVESASTQDALTMRSQLDOESGAIHPATQTSLOVRQRL 420
Db 361 PVOSHENFTAAATDLRYNNLTVESASTQDALTMRSQLDOESGAIHPATQTSLOVRQRL 420
QY 421 GSL 423
Db 421 GSL 423

RESULT 2
Q9NZV2
ID Q9NZV2 PRELIMINARY; PRT; 423 AA.
AC Q9NZV2;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)
DE TAJ-ALPHA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
RT Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-
RT Independent Cell Death.";
RL J. Biol. Chem. 275:15336-15342(2000).
DR EMBL; AF167555; AAF71828.1; -.
SQ SEQUENCE 423 AA; 46071 MW; BB7C9917132A4B2F CRC64;
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Query Match 98.9%; Score 2258; DB 4; Length 423;
Best Local Similarity 98.6%; Pred. No. 1.7e-200;
Matches 417; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
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QY 1 MALKVLEQEKFTFTLLVLLGYLSCKVTCTGDCRQOEFRDRSGNCVPCNQCQPGMELSK 60
Db 1 MALKVLEQEKFTFTLLVLLGYLSCKVTCTGDCRQOEFRDRSGNCVPCNQCQPGMELSK 60
QY 61 ECGFGYGEDAQCVTCRLHREFKEDWGQKPCLDCAVAVNRFOKANCATSDAICGDLPG 120
Db 61 ECGFGYGEDAQCVTCRLHREFKEDWGQKPCLDCAVAVNRFOKANCATSDAICGDLPG 120
QY 121 FYRKTLLVGFQDMQECVPCGDDPPPEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
Db 121 FYRKTLLVGFQDMQECVPCGDDPPPEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
QY 181 VLLALLILCVYKROFMKKPSWLSRSQDIQYNGSELSCFDRPQLHEYAHRAACCCRRD 240
Db 181 VLLALLILCVYKROFMKKPSWLSRSQDIQYNGSELSCFDRPQLHEYAHRAACCCRRD 240
QY 241 SVOTCGPVRLLPSMCCCEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Db 241 SVOTCGPVRLLPSMCCCEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
QY 301 CGEFSDAWPLMQNPMGDDNISFCDSYPCLTGEDIHSLNPELESSTSLDSSODLVGGAV 360
Db 301 CGEFSDAWPLMQNPMGDDNISFCDSYPCLTGEDIHSLNPELESSTSLDSSODLVGGAV 360
QY 361 PVOSHENFTAAATDLRYNNLTVESASTQDALTMRSQLDOESGAIHPATQTSLOVRQRL 420
Db 361 PVOSHENFTAAATDLRYNNLTVESASTQDALTMRSQLDOESGAIHPATQTSLOVRQRL 420
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Db 361 PVOSHENFTAAATDLRYNNLTVESASTQDALTMRSQLDOESGAIHPATQTSLOVRQRL 420
QY 421 GSL 423
Db 421 GSL 423

RESULT 3
Q9JJH6
ID Q9JJH6 PRELIMINARY; PRT; 416 AA.
AC Q9JJH6;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)
DE TROY.
GN TROY.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kojima T., Morikawa Y., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Senba E., Kitamura T.;
RT "TROY, a newly identified member of the tumor necrosis factor receptor
RT superfamily, exhibits a homology with Edar and is expressed in
RT embryonic skin and hair follicles";
RL J. Biol. Chem. 275:20742-20747(2000).
DR EMBL; AB040432; BAB03267.1; -.
SQ SEQUENCE 416 AA; 45265 MW; 9BDC7C7A2D6A9C47 CRC64;
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Query Match 68.3%; Score 1559.5; DB 11; Length 416;
Best Local Similarity 70.5%; Pred. No. 5.5e-136;
Matches 294; Conservative 34; Mismatches 84; Indels 5; Gaps 3;
```

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QY 1 MALKVLEQEKFTFTLLVLLGYLSCKVTCTGDCRQOEFRDRSGNCVPCNQCQPGMELSK 60
Db 1 MALKVLEQEKFTFTLLVLLGYLSCKVTCTGDCRQOEFRDRSGNCVPCNQCQPGMELSK 60
QY 61 ECGFGYGEDAQCVTCRLHREFKEDWGQKPCLDCAVAVNRFOKANCATSDAICGDLPG 120
Db 61 ECGFGYGEDAQCVTCRLHREFKEDWGQKPCLDCAVAVNRFOKANCATSDAICGDLPG 120
QY 121 FYRKTLLVGFQDMQECVPCGDDPPPEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
Db 121 FYRKTLLVGFQDMQECVPCGDDPPPEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
QY 181 VLLALLILCVYKROFMKKPSWLSRSQDIQYNGSELSCFDRPQLHEYAHRAACCCRRD 240
Db 181 VLLALLILCVYKROFMKKPSWLSRSQDIQYNGSELSCFDRPQLHEYAHRAACCCRRD 240
QY 241 SVOTCGPVRLLPSMCCCEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
Db 241 SVOTCGPVRLLPSMCCCEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
QY 301 CGEFSDAWPLMQNPMGDDNISFCDSYPCLTGEDIHSLNPELESSTSLDSSODLVGGAV 360
Db 301 CGEFSDAWPLMQNPMGDDNISFCDSYPCLTGEDIHSLNPELESSTSLDSSODLVGGAV 360
QY 361 PVOSHENFTAAATDLRYNN--TLVESASTQDALTMRSQLDOESGAIHPATQTSLO 415
Db 359 -ALESSGNVSESTDSPRHGDGTGTWVEQTTLAQDAQRTPSQGGWEDRENLLAMPTAQ 414

RESULT 4
Q9JLL3
ID Q9JLL3 PRELIMINARY; PRT; 416 AA.
AC Q9JLL3;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)
DE TAJ-ALPHA LONG.
```

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
 RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
 RT Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-
 RT Independent Cell Death.";
 RL J. Biol. Chem. 275:15336-15342(2000).
 DR EMBL; AF167552; AAF17825.1; -;
 SQ SEQUENCE 416 AA; 45294 MW; 19CA2F75DD7B9D49 CRC64;

Query Match 68.2%; Score 1557.5; DB 11; Length 416;
 Best Local Similarity 70.5%; Pred. No. 8.4e-136;
 Matches 294; Conservative 33; Mismatches 85; Indels 5; Gaps 3;

Qy 1 MALKVLEQEKTFFTLVLLGYLSCKVTCETGDCRQEQFRDRSGNCVPCNQCQPGMELSK 60
 Db 1 MALKVLPPLHRTVLFPAAILFLLHLACKVSCETGDCRQEQFRDRSGNCVLCQCGPGMELSK 60
 Qy 61 ECGFGYGEDAQCVCPRHFRFKEDWGFKCPCLDCAVNRFKANCATSDAICGDCPLG 120
 Db 61 ECGFGYGEDAQCVCPRHFRFKEDWGFKCPCLDCALVNRFORANCSTSDAVCGDCPLG 120
 Qy 121 FYRKTGLVGFQDMQVPCGDPDPPEPHCASKVNLVKIATSTASSPRDATALAIVICAT 180
 Db 121 FYRKTGLVGFQDMQVPCGDPDPPEPHCTSKVNLVKISSTVSSPRDATALAIVICAT 180
 Qy 241 SVQTCGPVRLPSCMCEACSPNPATLGGVHSAASLQARNAGPAGVMVPTFGSLTQSI 300
 Db 241 SAPMTGPVHLIPSLACCEARSAARAVLGGCLRSPTTLQERNPASVGNTPAPFGSVRSI 300
 Qy 301 CGEFSAMPPLMONGNIPSCDSYPELTGEDIHSLNPEL 341
 Db 301 CAEFSAMPPLMONGNIPSGDS-SLDCSYPELTGEDIHSLNPEM 340
 Qy 181 VLLALLILCVYCKRFMEKPSWLSRQDIQYNGSELSCLDRLPQHEHRAACQCRRD 240
 Db 181 VLLALLILCVYCKRFMEKPSWLSRQDIQYNGSELSCFDQPRLRHCAHRAACQYHRD 240
 Qy 301 CGEFSAMPPLMONGNIPSCDSYPELTGEDIHSLNPEL 341
 Db 301 CAEFSAMPPLMONGNIPSGDS-SLDCSYPELTGEDIHSLNPEM 340
 Qy 361 PVQSHENFTATDLRSYNN--TLVESASTQDALTMRSQDQESGAIHPATQTSILQ 415
 Db 359 -ALESSGNVSESTDSPRHGDTGTVEQTLAQDAQTPTSGGWDRENLMPTAFQ 414

RESULT 5
 Q90XW7
 ID Q90XW7 PRELIMINARY; PRT; 348 AA.
 AC Q90XW7
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE TNFRSF19.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hu S., Tamada K., Ni J., Vincenz C., Chen L.;
 RT "Characterization of TNFRSF19, a novel member of tumor necrosis factor
 RT receptor superfamily.";
 RL Genomics 62:103-107(1999).
 DR EMBL; AF173166; AAF19795.1; -;
 DR INTERPRO; IPR001368; -;
 DR PFAM; PF00020; TNFR_C6; 2.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
 DR PROSITE; PS50050; TNFR_NGFR_2; 1.
 SQ SEQUENCE 348 AA; 38450 MW; 013C799638F0E333 CRC64;

Query Match 42.8%; Score 977; DB 11; Length 214;
 Best Local Similarity 84.6%; Pred. No. 1.6e-82;
 Matches 176; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

Qy 1 MALKVLEQEKTFFTLVLLGYLSCKVTCETGDCRQEQFRDRSGNCVPCNQCQPGMELSK 60
 Db 1 MALKVLPPLHRTVLFPAAILFLLHLACKVSCETGDCRQEQFRDRSGNCVLCQCGPGMELSK 60
 Qy 61 ECGFGYGEDAQCVCPRHFRFKEDWGFKCPCLDCAVNRFKANCATSDAICGDCPLG 120
 Db 61 ECGFGYGEDAQCVCPRHFRFKEDWGFKCPCLDCALVNRFORANCSTSDAVCGDCPLG 120

Db 61 ECGFGYGEDAQVPCPRHRFKEDWGQKCKPCADCALVNRFRQANCSTHTSDAVCGDCLPG 120
QY 121 FYRKTLLVGFQDMCEVPCGPPPPYPHCASKVNLVKIATSTASSPRDTALAAYICSALAT 180
Db 121 FYRKTLLVGFQDMCEVPCGPPPPYPHCASKVNLVKIATSTASSPRDTALAAYICSALAT 180
QY 181 VLLALLILCVIYCKRQFMKKPSWSLRS 208
Db 181 VLLALLILCVIYCKRQFMKKPSKCLPS 208
RESULT 7
Q9JLL2 PRELIMINARY; PRT; 150 AA.
AC Q9JLL2
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE TAJ-BETAL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RA Eby M.T., Jasmin A., Kumar A., Sharma K., Chaudhary P.M.;
RT "TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
RT Activates the c-Jun N-terminal Kinase Pathway and Mediates Caspase-
RT Independent Cell Death.";
RL J. Biol. Chem. 275:15336-15342(2000).
DR EMBL; AF167554; AAF1827.1; -.
SQ SEQUENCE 150 AA; 16728 MW; 4A1B2E93AE7FF43 CRC64;

Query Match 31.8%; Score 725; DB 11; Length 150;
Best Local Similarity 82.6%; Pred. No. 2.1e-59;
Matches 123; Conservative 9; Mismatches 17; Indels 0; Gaps 0;
QY 1 MALKVLEQEKTFLLVLLGLYSCKVTCETGDCRQEFDRSGNCVPCNOCGPGMELSK 60
Db 1 MALKVPLHRTVLFALFLHLLACKVSCETGDCRQEFDRSGNCVLCQCGPGMELSK 60
QY 61 ECGFGYGEDAQVTCRLHRFKEDWGQKCKPCDCAVNVRFQKANCSDAICGDCPLG 120
Db 61 ECGFGYGEDAQVPCPRHRFKEDWGQKCKPCADCALVNRFRQANCSTHTSDAVCGDCLPG 120
QY 121 FYRKTLLVGFQDMCEVPCGPPPPYPHC 149
Db 121 FYRKTLLVGFQDMCEVPCGPPPPYPHC 149

RESULT 8
Q9R187 PRELIMINARY; PRT; 448 AA.
AC Q9R187;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE ECTODERMAL DYSPLASIA RECEPTOR.
GN EDAR OR DL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE-99364417; PubMed-10431242;
RA Headon D.J., Overbeek P.A.;
RT "Involvement of a novel Tnf receptor homologue in hair follicle
RT induction";
RL Nat. Genet. 22:370-374(1999).
DR EMBL; AF160502; AAD50425.1; -.
DR MGI; 1343498; Edar.

KW Receptor.
SQ SEQUENCE 448 AA; 48434 MW; FCCAF38F3D6BB971 CRC64;
Query Match 8.6%; Score 197; DB 11; Length 448;
Best Local Similarity 28.2%; Pred. No. 4.2e-10;
Matches 61; Conservative 32; Mismatches 83; Indels 40; Gaps 11;
QY 16 LVLVLLGYSCKVTCETGDCRQEFDRSGNCVPCNOCGPGMELSKCEGFG-YGEDAQCV 73
Db 13 LPVLVLSLMSARAEDSNCGENYHNQTTGLCQCCPCRPGEPEYMSCGYGTDDYGCV 72
QY 74 TCRHFRFKEDWGQKCKPCDCAVNVRFQKANC-----SATSDAICGDCPLPGFY-----RKT 125
Db 73 PCPAEKFSKG-GYOICRRHKDC---EGFFRATVLTPCDMENDAECGCLPGYYMLNRP 128
QY 126 KLGVFQDMCEVPCGPPPPYPHCASKVNLVKIATSTASSPRDTA-----L 170
Db 129 NIYG---MVCYSC-LLAPPNTKECVGATSGVSAHSSSTSGSTLSPFQHAHKELSGO 184
QY 171 AAVICSALATVL---LALLILCVIYCKRQFMKKPS 203
Db 185 ATALIAMSTIFIMATAIVLIIMFY----IMTKPS 216

RESULT 9
Q9UNE0 PRELIMINARY; PRT; 448 AA.
AC Q9UNE0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE ECTODYSPLASIN-A RECEPTOR PROTEIN.
GN EDAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE-99364416; PubMed-10431241;
RA Montreal A.W., Ferguson B.M., Headon D.J., Street S.L., Overbeek P.A.,
RT Zonana J.;
RT "Mutations in the human homologue of mouse dl cause autosomal
RT recessive and dominant hypohidrotic ectodermal dysplasia";
RL Nat. Genet. 22:366-369(1999).
DR EMBL; AF130988; AAD50076.1; -.
KW Receptor.
SQ SEQUENCE 448 AA; 48582 MW; AC8D61249D608439 CRC64;

Query Match 8.4%; Score 191; DB 4; Length 448;
Best Local Similarity 28.7%; Pred. No. 1.5e-09;
Matches 62; Conservative 30; Mismatches 84; Indels 40; Gaps 12;
QY 16 LVLVLLGYSCKVTCETGDCRQEFDRSGNCVPCNOCGPGMELSKCEGFG-YGEDAQCV 73
Db 13 LPVLVLSLMSARAEDSNCGENYHNQTTGLCQCCPCRPGEPEYMSCGYGTDDYGCV 72
QY 74 TCRHFRFKEDWGQKCKPCDCAVNVRFQKANC-----SATSDAICGDCPLPGFY-----RKT 125
Db 73 PCPAEKFSKG-GYOICRRHKDC---EGFFRATVLTPCDMENDAECGCLPGYYMLNRP 128
QY 126 KLGVFQDMCEVPCGPPPPYPHCASKVNLVKI-----ASTASSPRDTA-----L 170
Db 129 NIYG---MVCYSC-LLAPPNTKECVGATSGASANFFGTSGSTLSPFQHAHKELSGO 184
QY 171 AAVICSALATVL---LALLILCVIYCKRQFMKKPS 203
Db 185 ATALIAMSTIFIMATAIVLIIMFY----IMTKPS 216

RESULT 10

```
Q9UND9
ID Q9UND9 PRELIMINARY; PRT; 448 AA.
AC Q9UND9;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE ECTODYSPLASIN-A RECEPTOR PROTEIN.
GN EDAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99364416; PubMed=10431241;
RA Monreal A.W., Ferguson B.M., Headon D.J., Street S.L., Overbeek P.A.,
RA Zonana J.;
RT "Mutations in the human homologue of mouse dl cause autosomal
RT recessive and dominant hypohidrotic ectodermal dysplasia.";
RL Nat. Genet. 22:366-369(1999).
DR EMBL; AF130996; AAD50077.1; -.
DR EMBL; AF130990; AAD50077.1; JOINED.
DR EMBL; AF130991; AAD50077.1; JOINED.
DR EMBL; AF130992; AAD50077.1; JOINED.
DR EMBL; AF130993; AAD50077.1; JOINED.
DR EMBL; AF130994; AAD50077.1; JOINED.
DR EMBL; AF130995; AAD50077.1; JOINED.
KW Receptor.
SQ SEQUENCE 448 AA; 48572 MW; AC8FB0F79CB255EA CRC64;

Query Match 8.4%; Score 191; DB 4; Length 448;
Best Local Similarity 28.7%; Pred. No. 1.5e-09;
Matches 62; Conservative 30; Mismatches 84; Indels 40; Gaps 12;

Qy 16 LVLVLYLCKVCTGTGDCRQEFDR-SGNCVPCNQCGPMELSKCEGFG-YGEDACV 73
Db 13 LPVLVSLMCSARAEYSNGENYYNQTLGCEQPCGPGPEEYLSGCGYTKDEYGV 72
Qy 74 TRLHFKEDMGFOCKPCLDCAVNRFQKNC-----SATDAICGDCGLPGFY----RKT 125
Db 73 PCPAEKFSK-GYQICRRHKC---EGFRATVLTGDMENDAECCPLGMYMLNRP 128
Qy 126 KLVGQDMCEVPCGDPPEYEPHCASKVNLVKI-----ASTASSPRDTA-----L 170
Db 129 NIYG---MVCYSC-LLAPNTKECVGATSGASANPPTSGSSTLSPFQHAHKLSGQGH 184
Qy 171 AAVICSALATVL---LALLILCVYCKQFMKPKS 203
Db 185 ATALIAMSTIFMAIAIVLIMFY---ILTKRPS 216

RESULT 11
Q9PVD4 PRELIMINARY; PRT; 387 AA.
ID Q9PVD4;
AC Q9PVD4;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE P75-LIKE TRANSMEMBRANE PROTEIN FULLBACK.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC xenopodinae; xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Hick E., Sun B.I., Collins-Racie L., LaVallie E., Sive H.L.;
RT "Identification and Characterization of fullback, a Novel Posteriorly-
RT Expressed Xenopus Gene.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF131890; AAD54072.1; -.
DR HSSP; P07174; INGR.
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DR INTERPRO; IPR000488; -.
DR INTERPRO; IPR001368; -.
DR PFAM; PF00020; TNFR_C6; 4.
DR PFAM; PF00531; death; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_3.
DR PROSITE; PS00117; DEATH_DOMAIN; 1.
DR PROSITE; PS00500; TNFR_NGFR_2; 4.
KW Transmembrane.
SQ SEQUENCE 387 AA; 42066 MW; 1A386A239C7C8A82 CRC64;

Query Match 7.5%; Score 170.5; DB 13; Length 387;
Best Local Similarity 23.6%; Pred. No. 1e-07;
Matches 69; Conservative 35; Mismatches 93; Indels 95; Gaps 15;

Qy 16 LVLVLYLCKVCTGTGDCRQEFDRSGNCGVPCNQCGPMELSKCEGFGYGEDACQVTC 75
Db 12 LLLLSKISAEADVCSG-----LYTNSGKC--CSLCPAGGVVPPCG---DSDTKCEPC 60
Qy 76 RLHREKEDWGQ-----KCKPCLDCAVNRFQKNCASATSDAIC-----GDC 117
Db 61 -----IENSTFSDVRSKAKCOPCTCQSPSLTLESNCTREODTVORCPEROYLDNGIC 115
Qy 118 LP-----GFYRKTKLVGFQDMCEVPC-----G 139
Db 116 LPCQLCSKRGHVWSQTHKNKTVCOLCSSGFYSEVK---SSSPCLPCRTECKETEVOIG 172
Qy 140 DPPPPEPHCASK-VNLVK-----IATASS-----PRDTA--LAAVICSALATVLLALL 186
Db 173 DCVPQHDILCMQDKVPIILKRTGEGNGTSAGSPHPIDQNSKNIIPVYCSILAAVVVGLI 232
Qy 187 ILCVYCKRQFMKPKPSWLSRSDI--QVNGSELS-----CLDRPOLHAYH 231
Db 233 AYVAFKCYTCQKQAKARAGELATSTEGEKLNDSGVFLDTHSLQEPNH 284

RESULT 12
Q9N092 PRELIMINARY; PRT; 430 AA.
ID Q9N092;
AC Q9N092;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last annotation update)
DE UNNAMED PORTIN PRODUCT.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB046039; BAB01621.1; -.
SQ SEQUENCE 430 AA; 45850 MW; BA8DE92593E1E859 CRC64;

Query Match 6.3%; Score 144.5; DB 6; Length 430;
Best Local Similarity 21.3%; Pred. No. 2.8e-05;
Matches 57; Conservative 29; Mismatches 83; Indels 99; Gaps 8;

Qy 51 QCGPMELSKCEGFGYGEDACQVTCRLHREKEDWGFGKPCPLDCAVNRFQKNCASATS 110
Db 31 QCPPG-----EEDLPNGOGTLCRPPCTTSAAGSSPCQPHARCSLQRRLAQVGTATQ 86
Qy 111 DAICGDCGLPGFYRKTKLVGFQDMCEVPCGDPPEYEPHCASKVNL-----VK 157
Db 87 DTLCGDCWPGWFG-----PWGVPVPCQPSWAPLGIHGCDENGRARRGVE 133
Qy 158 IATASS-----PRDTALA-AVICSALATVLLALLILCVYCKRQFMKPK 201
```

```
Db 134 VAAGASSGGETROPNGTRAGGPEETAQAQAVI--AIVPVFLMGLLILVC-----183
QY 202 PSWSLSRQDIQYNGSELSCLDRLQHEHYAHRACCCQRRDSVQTCGVPRLPLSMCCBEACS 261
Db 184 -----NLLKRGYHCTAHK-----EVG 200
QY 262 PNPATLGGVHSAASLQARNAGPAGEMV 289
Db 201 PPGGGGGINPAYRTDVEDNIGVLV 228

RESULT 13
ID Q920W1 PRELIMINARY; PRT; 417 AA.
AC Q920W1;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE NERVE GROWTH FACTOR RECEPTOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A;
RX MEDLINE=99077793; PubMed=9857182;
RT Tuffreau C., Benjean J., Blondel D., Kieffer B., Flaman A.;
RT "Low-affinity nerve-growth factor receptor (p75NTR) can serve as a
RL receptor for rabies virus.";
RL EMBO J. 17:7250-7259(1998).
DR HMBL; AF105292; AAD17943.1; -
DR HSSP; P07174; INGR
DR INTERPRO; IPR000488; -
DR INTERPRO; IPR000561; -
DR INTERPRO; IPR000734; -
DR INTERPRO; IPR001368; -
DR PFAM; PF00020; TNFR_c6; 4.
DR PFAM; PF00531; death; 1.
DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
KW Receptor.
SQ SEQUENCE 417 AA; 44686 MW; 5D7A4510DB8AF9B2 CRC64;
```

```
QY 7 LEQKTEFTLLVLGLG--YLSCKVTCTGDCRQQRDRSGNCVPCNQCQGMELSKCEGF 64
Db 1 MDRLRLLLLLLLGVSFGGAKCTSGT-----MYTHSGEC--CKACNLGEGVAQPCG- 51
QY 65 GYGDAOCVTCRLHREFD--WGFKCKPCLDCAVNVRFKANCATSDAICGDCPLPGFY 122
Db 52 --ANQTVCEPCLDVTSVDVVSATEPCPKTECIGL--QSMSPCCEADDAVC--RCSTGYI 107
QY 123 RKTKLVGFQDME-----CVPCCGPPPPYPHPCASKYNLV-----KIATASSPRDTAL 170
Db 108 -----QDEETCEACSCVG--VSGSLVFCQDKQNTVCEECECTYSDEANHVDPC 158
QY 171 AAVTCSALATVLLALLILCVIYKRRQMEKKPSWSLSRQDIQYNGSELSCLDRLQHEHYA 230
Db 159 PCTVCEDTERQDLRE----CTPWADAEEIEPGRWITRSTPPE--GSDVT---TPSTQE-- 207
QY 231 HRACCQCRDSVQTCGVPV--LLPSMCCCEACSPNPATLGGVHSAASLQARNAGPAGEMV 289
Db 208 -----PEAPPERDLIATVAD-----TVTVMGSSQPVVTR--GTADNLI 245
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QY 290 PTFGSLTQSIGCEFS-----DAMPLQNMQPMGGDNISFCDSYPBLTGTEDIHSLNPELESST 345
Db 246 PVYCSILAAVVGVLVAYIAFKRWNSCKQNKQGANSPVNVQTPPPECKLHS-----DSGI 300
QY 346 SLDSSNQDLVGGAVPVQSHSENFTAAATDLRYNNVTLVESASTQDALTWRSQLDQ 400
Db 301 SVDSQSLHD-----QOHTQ--TASAQALKGDNLYSSL-----PLTKREEVEK 342

RESULT 14
ID O14865 PRELIMINARY; PRT; 426 AA.
AC O14865;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE DEATH RECEPTOR 3 BETA.
GN DR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98113360; PubMed=9446802;
RA Warzocha K., Ribeiro P., Charlot C., Renard N., Colffier B.,
RA Salles G.;
RT "A new death receptor 3 isoform: expression in human lymphoid cell
RT lines and non-Hodgkin's lymphomas.";
RL Biochem. Biophys. Res. Commun. 242:376-379(1998).
DR EMBL; AF026070; AAC39556.1; -
DR HSSP; P19438; INCF.
DR INTERPRO; IPR000488; -
DR INTERPRO; IPR000561; -
DR INTERPRO; IPR001368; -
DR PFAM; PF00020; TNFR_c6; 2.
DR PFAM; PF00531; death; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
SQ SEQUENCE 426 AA; 45950 MW; 371AA7F16AD29C16 CRC64;
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QY 34 CROQEFDRDRSGNC--VPCNQC--PGMELSKCEGFGYGEDAQCVCVTRLHFRKEDMGFKC 89
Db 95 CDEQASQVALENCASAVADTRCGCKPGWV--EC-----QVSCVSSSPF-----YC 138
QY 90 KPCLDCAVNVRFKANCATSDAICGDCPLPGFYRKYTKLVGFQDMCEVCPCGDPPEPHC 149
Db 139 QPCLDCCGALHRRHRLCLCS--RRDTCGTCCLPGFYE-----HGDGVCVSCPTPPP----- 184
QY 150 ASKVNVLKVIATSSPRDTALAAVICSAL-----ATVLLALLILCVIYKRRQFMEKK 201
Db 185 -----SLAGAPNGAVQSAVPLSVAGRGVGVFWVQVLLAGLVVPLL----- 225
QY 202 PSWSLSRQDIQYNGSELSCLDRLQHEHYAHRACCCQRRDSVQTCGVPRLPLSMCCBEACS 257
Db 226 -----GATLT-----VTYRH-----CWPHK--PLVTADEAGM 250
QY 258 EACSPNPATLGGVHSAASLQ 279
Db 251 EALTTPPPATHLSPLDSAHLLA 272

RESULT 15
ID O72735 PRELIMINARY; PRT; 186 AA.
AC O72735;
```


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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 16, 2001, 21:06:00 ; Search time 30.21 Seconds

(without alignments)
478.781 Million cell updates/sec

Title: US-09-380-276A-8

Perfect score: 2283

Sequence: 1 MALKVLLLEQKFTTLLVLL.....AIHPATQTSLOVRORLGLSL 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_36:*

- 1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT:*
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- 20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2278	99.8	423	20 W85724	Novel protein (Clo
2	2267	99.3	423	19 W0387	Amino acid sequenc
3	2258	98.9	423	20 W93581	Human HAPO4-alpha
4	2237	98.0	417	20 W98146	Human TRAIN-R. Ho
5	2230	97.7	417	19 W0386	Amino acid sequenc
6	1557.5	68.2	416	20 W93579	Mouse HAPO4-alpha
7	1544.5	67.7	328	20 Y06400	Human NTR-5 recept
8	977	42.8	214	20 Y06522	Mouse STRIP1 (Tan
9	977	42.8	214	20 W98145	Mouse TRAIN-R (lon
10	977	42.8	214	20 W93580	Mouse HAPO4-alpha
11	869	38.1	210	20 Y22223	Human TNFR superfa
12	854	37.4	150	20 W98148	TRAIN-R short, sol

13	783	34.3	160	20 Y06399	Mouse NTR-5 recept
14	725	31.8	150	20 Y06523	Mouse STRIP2 (Tan
15	725	31.8	150	20 Y22224	Mouse TNFR superfa
16	725	31.8	150	20 W98144	Mouse TRAIN-R (Sho
17	725	31.8	150	20 W93583	Mouse HAPO4-gamma
18	725	31.8	150	20 Y77465	Murine Rank-like p
19	480	21.0	231	21 Y77468	Human Rank-like pr
20	261.5	11.5	109	20 W93582	Rat rAPO4-alpha pr
21	244	10.7	77	21 Y77467	Human Rank-like pr
22	192.5	8.4	132	21 Y77466	Human Rank-like pr
23	179	7.8	30	20 W98147	TRAIN-R secreted f
24	159	7.0	438	16 R81882	Plasmid pDC406/OX4
25	159	7.0	438	19 W48976	OX40/FC mutein. C
26	150	6.6	206	16 R81881	Mouse type-II memb
27	150	6.6	206	19 W48977	Mouse OX40 extrace
28	146.5	6.4	1801	19 W50895	Rat laminin B2 cha
29	144	6.3	1104	17 R94957	NF-X1 DNA-binding
30	142	6.2	95	20 W93584	Mouse HAPO4-beta p
31	140.5	6.2	408	20 Y41111	Human TANGO 129 (T
32	140.5	6.2	430	20 Y41110	Human TANGO 129 (T
33	140.5	6.2	430	21 Y70785	Human tumour necro
34	140	6.1	425	21 Y92370	p75-NTR (neurotrop
35	137	6.0	1798	19 W50896	Human laminin B2 c
36	136	6.0	625	19 W83200	Murine osteoclast
37	136	6.0	625	19 W69958	Murine NF-KB recep
38	136	6.0	625	19 W68294	Murine NF-KB recep
39	136	6.0	625	21 Y59509	OBM binding protei
40	136	6.0	625	21 Y53649	A mouse receptor a
41	134	5.9	186	15 R62655	Cowpox virus pst I
42	134	5.9	307	18 W33358	TBP(20-161)/hcg-be
43	134	5.9	1764	10 P91672	Primary amino acid
44	134	5.9	1776	19 W50894	Mouse laminin B1 c
45	133.5	5.8	2050	20 W73499	Von Willebrand fac

ALIGNMENTS

RESULT 1

W85724

ID W85724 standard; Protein; 423 AA.

XX W85724;

XX AC

XX DT 27-SEP-1999 (first entry)

XX DE Novel protein (Clone AX92_3).

XX KW Polynucleotide; protein; nutrition; cytokine; cell proliferation;

XX KW cell differentiation; immunostimulation; immunosuppression;

XX KW haematopoiesis regulation; tissue growth; activin; inhibin;

XX KW chemotaxis; chemokinesis; haemostasis; thrombolysis; receptor;

XX KW ligand; anti-inflammatory; tumour suppression; gene therapy.

XX OS Homo sapiens.

XX PN WO9920644-A1.

XX PD 29-APR-1999.

XX PF 16-OCT-1998; 98WO-US22034.

XX PR 18-OCT-1997; 97US-0955557.

XX PA (GEMY) GENETICS INST INC.

XX PI Agostino MJ, Bowman MR, Evans C, Jacobs K, Lavallie ER;

XX PI McCoy JM, Merberg D, Racie LA, Spaulding V, Treacy M;

XX DR WPI; 1999-288272/24.

XX DR N-PSDB; X08689.

XX PT New polynucleotides encoding secreted human proteins

XX PS Claim 32: Page 117-118; 136pp; English.

XX CC The new human secreted proteins are encoded by polynucleotides

CC obtained from human placenta, adult testes, fetal kidney, fetal

CC brain, adult brain, adult brain and adult blood cDNA libraries.

CC The polynucleotides and proteins are predicted to have biological

CC activities which would make them suitable for treating, preventing or

CC ameliorating medical conditions in humans and animals. Suggested

CC activities include nutritional activity, cytokine and cell

CC proliferation/differentiation activity, immune stimulating (e.g. as

CC vaccines) or suppressing activity, haematopoiesis regulating

CC activity, tissue growth activity, activin/inhibin activity,

CC chemotactic/chemokinetic activity, haemostatic and thrombolytic

CC activity, receptor/ligand activity, anti-inflammatory activity,

CC adherin/tumour invasion suppressor activity, and tumour inhibition

CC activity. The polynucleotides are also stated to be useful for gene

CC therapy. The sequences identified by a secretory leader

CC sequence motif in the polynucleotide and it is thought that the

CC encoded proteins have biological activity by virtue of their secreted

CC nature. This polypeptide was encoded by a clone designated AX92_3

CC (See X08689).

XX SQ Sequence 423 AA;

Query Match 99.8%; Score 2278; DB 20; Length 423;

Best Local Similarity 99.8%; Pred. No. 2.1e-201;

Matches 422; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALKVLEQEKFTFTLLVLLGLYSCKVTCTGDCRQOEFRDRSGNCVPCNQCGPMELSK 60

DB 1 malvkllleqektfttllvllglylsckvtcetgdcrgqefdrsgncvpcnqcgpmelsk 60

QY 61 ECGFGYGEDAQCVTCRLHRFKEDWGQKPCLDCAVNRFKANCSDATCGDCLPG 120

DB 61 ecgfgygedaqcvctcrlhrfkedwgfqckpcldcavvnrfkancsatsdaicgdcclpg 120

QY 121 FYRKTKLGVFQDMECVPCGPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

DB 121 fyrktklvgfmdmecvpcgppppypchcaskvnlvkiastassprdtalaavicsalat 180

QY 181 VLLALLILCVYCKRQFMCKEPPSPATILGCGVHSAALQARNAGPAGEMVPTFFGSLTQSI 240

DB 181 vllallilcvyckrqfmeckpsspatilgcgvhsaalqarnagpagemvptffgsltqsi 240

QY 241 SVOTCGPVRLLPSMCCCEACSPNPATILGCGVHSAALQARNAGPAGEMVPTFFGSLTQSI 300

DB 241 svotcgpvrllpsmcceacspnpatilgcgvhsaalqarnagpagemvptffgsltqsi 300

QY 301 CGEFSDAWPLMQNPMDGDNISFCDSYPELTGEDIHSLNPELESSTSLDSSNODLVGGAV 360

DB 301 cgefsdawplmqnmpmdgdnisfcdsypeeltgedihslnpelesstslsdsnsodlvvgav 360

QY 361 PVQSHSENFTAAATDLRYNNLTVESASTQDALTMRSQDQESGAIHPATQTSLOVRQL 420

DB 361 pvqshsenftaatdlrnyntlvesastqdaltmrsqdqesgaiihpatqtslvrql 420

RESULT 2

ID W70387

AC W70387 standard; Protein: 423 AA.

AC W70387;

DT 02-DEC-1998 (first entry)

XX DE Amino acid sequence of human beta-OAF065.

XX

KW Human; beta-OAF065; stroma cell; antibody; inflammatory;

XX cytokine-mediated disease; rheumatism; ulcerative colitis.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 223

FT /note= "encoded by AGA"

FT Misc-difference 224

FT /note= "encoded by CCT"

XX WO9838304-A1.

XX 03-SEP-1998.

XX 26-FEB-1998; 98WO-JP00799.

XX 27-FEB-1997; 97JP-0043143.

XX (ONOV) ONO PHARM CO LTD.

XX Fukushima D, Konishi M, Tada H;

XX WPI; 1998-481205/41.

XX N-PSDB; V33362.

XX Membrane polypeptide expressed by human stroma cells, and antibodies

PT recognising it - for treatment of inflammatory and other

PT cytokine-mediated diseases.

XX Disclosure; Pages 37-49; 54pp; Japanese.

XX This is the amino acid sequence of the human beta-OAF065, used in

CC the method of the invention. The process involves the use of peptides

CC expressed by stroma cells, and its antibodies are used for in the

CC prevention and treatment of inflammatory and other cytokine-mediated

CC diseases such as rheumatism, ulcerative colitis.

XX SQ Sequence 423 AA;

Query Match 99.3%; Score 2267; DB 19; Length 423;

Best Local Similarity 99.5%; Pred. No. 2.2e-200;

Matches 421; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MALKVLEQEKFTFTLLVLLGLYSCKVTCTGDCRQOEFRDRSGNCVPCNQCGPMELSK 60

DB 1 malvkllleqektfttllvllglylsckvtcetgdcrgqefdrsgncvpcnqcgpmelsk 60

QY 61 ECGFGYGEDAQCVTCRLHRFKEDWGQKPCLDCAVNRFKANCSDATCGDCLPG 120

DB 61 ecgfgygedaqcvctcrlhrfkedwgfqckpcldcavvnrfkancsatsdaicgdcclpg 120

QY 121 FYRKTKLGVFQDMECVPCGPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180

DB 121 fyrktklvgfmdmecvpcgppppypchcaskvnlvkiastassprdtalaavicsalat 180

QY 181 VLLALLILCVYCKRQFMCKEPPSPATILGCGVHSAALQARNAGPAGEMVPTFFGSLTQSI 240

DB 181 vllallilcvyckrqfmeckpsspatilgcgvhsaalqarnagpagemvptffgsltqsi 240

QY 241 SVOTCGPVRLLPSMCCCEACSPNPATILGCGVHSAALQARNAGPAGEMVPTFFGSLTQSI 300

DB 241 svotcgpvrllpsmcceacspnpatilgcgvhsaalqarnagpagemvptffgsltqsi 300

QY 301 CGEFSDAWPLMQNPMDGDNISFCDSYPELTGEDIHSLNPELESSTSLDSSNODLVGGAV 360

DB 301 cgefsdawplmqnmpmdgdnisfcdsypeeltgedihslnpelesstslsdsnsodlvvgav 360

QY 361 PVQSHSENFTAAATDLRYNNLTVESASTQDALTMRSQDQESGAIHPATQTSLOVRQL 420

DB 361 pvqshsenftaatdlrnyntlvesastqdaltmrsqdqesgaiihpatqtslvrql 420

QY 421 GSL 423
 Db 421 gsl 423

RESULT 3
 ID W93581 standard; Protein; 423 AA.
 AC W93581;
 XX
 DT 18-JUN-1999 (first entry)
 DE Human hAPO4-alpha protein.
 XX
 KW Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
 KW developmental abnormality; gestational abnormality; prostate cancer;
 KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
 KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
 KW apoptosis; human; APO4-alpha.
 XX
 OS Homo sapiens.
 XX
 PN WO9911791-A2.
 PD 11-MAR-1999.
 XX
 PF 04-SEP-1998; 98WO-US18393.
 XX
 PR 05-SEP-1997; 97US-0924634.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Chaudhary PM;
 XX
 DR WPI; 1999-205191/17.
 DR N-PSDB; X23415.
 XX
 PT New Tumor Necrosis Factor family receptor polypeptides and ligands -
 PT useful for diagnosis and treatment of prostate cancer and
 PT developmental or gestational abnormalities
 XX
 PS Claim 1; Fig 7C; 156pp; English.
 XX
 CC This invention describes isolated Tumor Necrosis Factor (TNF) family
 CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active
 CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
 CC their active fragments. APO4 is useful for diagnosing prostate cancer
 CC by determining levels of APO4 in an individual. Prostate cancer can also
 CC be treated using APO4 selective binding agents linked to a therapeutic
 CC moiety. APO4 polypeptides are also useful for identifying selective
 CC binding agents, useful in diagnosis/treatment of disease by binding of
 CC agents to the polypeptide/active fragment which is extracellular, or
 CC expressed on the cell surface. The binding is preferably performed in
 CC vivo. APO4 polypeptides/active fragments are also useful for screening
 CC for agonists and antagonists by binding and observing the change in APO4
 CC activity. Effective pharmacological agents useful in diagnosis or
 CC treatment of disease are also identified using APO4 polypeptides/active
 CC fragments and APO4 signal transducer molecules that specifically interact
 CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4
 CC activity. The method is performed in vivo or in vitro. APO polypeptides
 CC are all useful as immunogens for preparing antibodies. APO4 is also
 CC useful for diagnosis/treatment of developmental or gestational
 CC abnormalities. APO8 was transfected to human breast carcinoma cell line
 CC MCF-7, and induced apoptosis.
 XX
 SQ Sequence 423 AA;

Query Match 98.9%; Score 2258; DB 20; Length 423;
 Best Local Similarity 98.6%; Pred. No. 1.5e-199;
 Matches 417; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MALKVLEQEKTFFTLLVLLGYLSCKVTCTGDCRQEQFRDRSGNCVPCNOCGPGMELSK 60
 Db 1 malkvleqektfllvllgylsckvtctesgdcrcqefdrsgncvpcncgpgmelsk 60

QY 61 ECGFGYGEDAQCVTCLRLHFKEDWGFQCKPCLDCAVVNRFOKANCATSADAICGDCLPG 120
 Db 61 ecgfgygedaqcvtclrlhfkedwgfqckpcldcavvnrfgkancsatsdaicgdcipg 120

QY 121 FYRKTLYGFQDMCEVPCGDDPPPPYEPHCASKVNLVKIATASSPRDTALAAVICSALAT 180
 Db 121 fyrktlygfqdmcevcpgddppppypchcaskvnlvkiatassprdtalaavicsalat 180

QY 181 VLLALLILCVYCKRQFMEKKPSWLSRSDIOYNGSELSCLDRLPOLHEVYAHRACCQCRRD 240
 Db 181 vllallilcvyckrqfmeekpswlsrsqdiqyngselscldrlpolhevyahracccqrrd 240

QY 241 SVQTGCPVRLPSCMCEBACSPNATLGGVHSAASLAARNAGPAGEMVPTFFGSLTQSI 300
 Db 241 svqtgcpvrlpsscmeceacspnatlggvhsaaslaarnagpagemvptffgsltqsi 300

QY 301 CGEFS DANPLMONGDNISFCDSYPPELTGEDIHSLNPELESSTSLDSNSSQDLVGAV 360
 Db 301 cgefsdawnplmqnmgdgnisfcdsypelgtgedihslnpelesstslsdsnssqdlvgav 360

QY 361 PVQSHSENFTATDLRYNNTLVESASTQDALTMRSQLDOESGAIHPATQTSLOVRQL 420
 Db 361 pvqshsenftaatdlrynntlvesastqtdaltmrsqldoesgaihpatqtslqvrrql 420

QY 421 GSL 423
 Db 421 gsl 423

RESULT 4
 W98146
 ID W98146 standard; Protein; 417 AA.
 XX
 AC W98146;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE Human TRAIN-R.
 XX
 KW TRAIN-R; receptor; human; tumour necrosis factor receptor;
 KW agonist; antagonist; cancer; immunological disease; therapy;
 KW cytosolic.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21 /note= "signal peptide"
 FT Protein 22..417 /note= "mature protein"
 FT Domain 26..173 /note= "extracellular domain"
 FT Domain 174..190 /note= "transmembrane domain"
 FT Domain 191..417 /note= "cytoplasmic domain"
 XX
 PN WO9913078-A1.
 XX
 PD 18-MAR-1999.
 XX
 PF 11-SEP-1998; 98WO-US19030.
 XX
 PR 06-MAY-1998; 98US-0084422.
 PR 12-SEP-1997; 97US-0058631.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Hession C, Tschopp J;

XX WPI; 1999-229238/19.
 DR N-PSDB; X24978.
 XX
 PT New cysteine-rich tumor necrosis factor receptor
 PS
 XX Claim 2; Page 26; 30pp; English.
 CC The present sequence is a novel human cysteine-rich tumour
 CC necrosis factor receptor family member termed TRAIN-R that is
 CC expressed at low levels in every tissue and cell line tested thus
 CC far, with higher expression detected in heart, prostate, ovary,
 CC testis, peripheral blood lymphocytes, thyroid and adrenal gland.
 CC Cell death can be induced by administering an agent capable of
 CC inhibiting the binding of TRAIN-R to its ligand. A claimed method
 CC of treating, or reducing, the advancement, severity or effects of
 CC an immunological disease in a mammal comprises administering a
 CC pharmaceutical composition which comprises a TRAIN-R blocking agent,
 CC e.g. soluble TRAIN-R. TRAIN-R can be fused to an immunoglobulin to
 CC produce a fusion protein which may be targeted to various sites.
 CC It can be used in binding assays, and to identify antagonists and
 CC agonists. Anti-TRAIN-R antibodies can be used to reduce the
 CC severity of an immune response or to treat cancer. TRAIN-R
 CC blocking agents can also be used to reduce the severity or effects
 CC of an immunological disease (all claimed).
 XX
 SQ Sequence 417 AA;

Query Match 98.0%; Score 2237; DB 20; Length 417;
 Best Local Similarity 99.3%; Pred. No. 1.2e-197;
 Matches 412; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MALKVLEQEKTFLLVLLGLYSCKVCTGTGCRQEFDRDRSGNCVPCNQCSPGMELSK 60
 DB 1 malkvleqektftllvlllgylsckvtcetgcrqefdrdrsgncvpcnqcspgmelsk 60
 QY 61 ECGFGYGEDAQVCTCLRHREKEDWGFQKCKPCLDCAVNNRFQKANCSDATCGDCLPG 120
 DB 61 ecgfgygedaqvctclrhrfkedwgfqkckpcldcavnnrfqkancsatsdaicgdcplg 120
 QY 121 FYRKTUFGQDMECVPCGDPDPPEPHCASKVNLVKIASTASPRDTALAAVICSALAT 180
 DB 121 fyrktklvgfdmecnvpcgdpdppephcaskvnlvkiastassprdtalaavicsalat 180
 QY 181 VLLALLTLVYCKRQPMKKPSLSRSDIOYNGSELSCLDRLPQLHEYAHRAACCCRRD 240
 DB 181 vllalltlvlyckrqpmekppswlsrsdiongselscldrpqlheyaahracccrrd 240
 QY 241 SVQTCGPVRLLPSCMCEEACSPNPATLGCYVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
 DB 241 svtcgvpvrlpmsmceeeacspnpatlgcgvhsaaslgarnagpagemvptffgsltqsi 300
 QY 301 CGEFSDAWPLMQNPMGDNISFCDSPYELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
 DB 301 cgefsdawlmpnqpmgdnisfcdsyelpeltgedihslnpelesstsldsnsqdlvggav 360
 QY 361 PVQSHSENFTAATDLSRYNNLTVESASTQDALTMRSLQDQESGAIHPATQTSILQ 415
 DB 361 pvqshsenftaatdlsrynnltvesastqdaltrmsrlqdesgailhpatqtsilq 415

RESULT 5
 W70386
 ID W70386 standard; Protein; 417 AA.
 XX
 AC W70386;
 XX
 DT 02-DEC-1998 (first entry)
 XX
 DE Amino acid sequence of human alpha-OAF065.
 XX
 KW Human; alpha-OAF065; stroma cell; antibody; inflammatory;

KW cytokine-mediated disease; rheumatism; ulcerative colitis.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 223 /note= "encoded by AGA"
 FT Misc-difference 224 /note= "encoded by CCT"
 FT
 XX WO9838304-A1.
 PN
 XX
 XX 03-SEP-1998.
 PD
 XX 26-FEB-1998; 98WO-JP00799.
 PF
 XX 27-FEB-1997; 97JP-0043143.
 PR
 XX (ONOV) ONO PHARM CO LTD.
 PA Fukushima D, Konishi M, Tada H;
 PI
 XX WPI; 1998-481205/41.
 DR N-PSDB; V33361.
 XX
 PT Membrane polypeptide expressed by human stroma cells, and antibodies
 PT recognising it - for treatment of inflammatory and other
 PT cytokine-mediated diseases.
 XX
 PS Claim 1; Pages 28-30; 54pp; Japanese.
 XX
 XX This is the amino acid sequence of the human alpha-OAF065, used in
 CC the method of the invention. The process involves the use of peptides
 CC expressed by stroma cells, and its antibodies are used for in the
 CC prevention and treatment of inflammatory and other cytokine-mediated
 CC diseases such as rheumatism, ulcerative colitis.
 XX
 SQ Sequence 417 AA;

Query Match 97.7%; Score 2230; DB 19; Length 417;
 Best Local Similarity 99.5%; Pred. No. 5.4e-197;
 Matches 413; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MALKVLEQEKTFLLVLLGLYSCKVCTGTGCRQEFDRDRSGNCVPCNQCSPGMELSK 60
 DB 1 malkvleqektftllvlllgylsckvtcetgcrqefdrdrsgncvpcnqcspgmelsk 60
 QY 61 ECGFGYGEDAQVCTCLRHREKEDWGFQKCKPCLDCAVNNRFQKANCSDATCGDCLPG 120
 DB 61 ecgfgygedaqvctclrhrfkedwgfqkckpcldcavnnrfqkancsatsdaicgdcplg 120
 QY 121 FYRKTUFGQDMECVPCGDPDPPEPHCASKVNLVKIASTASPRDTALAAVICSALAT 180
 DB 121 fyrktklvgfdmecnvpcgdpdppephcaskvnlvkiastassprdtalaavicsalat 180
 QY 181 VLLALLTLVYCKRQPMKKPSLSRSDIOYNGSELSCLDRLPQLHEYAHRAACCCRRD 240
 DB 181 vllalltlvlyckrqpmekppswlsrsdiongselscldrpqlheyaahracccrrd 240
 QY 241 SVQTCGPVRLLPSCMCEEACSPNPATLGCYVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
 DB 241 svtcgvpvrlpmsmceeeacspnpatlgcgvhsaaslgarnagpagemvptffgsltqsi 300
 QY 301 CGEFSDAWPLMQNPMGDNISFCDSPYELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV 360
 DB 301 cgefsdawlmpnqpmgdnisfcdsyelpeltgedihslnpelesstsldsnsqdlvggav 360
 QY 361 PVQSHSENFTAATDLSRYNNLTVESASTQDALTMRSLQDQESGAIHPATQTSILQ 415
 DB 361 pvqshsenftaatdlsrynnltvesastqdaltrmsrlqdesgailhpatqtsilq 415

CC clone (see x59346). Homology to osteoprotegerin suggests that NTR-5
 CC is involved in the regulation of bone mass, and may be useful for
 CC regulating development, proliferation and death of osteoblast or
 CC osteoclast cells or for regulating muscle metabolism, and that it
 CC may be implicated in muscle diseases or disorders. A host-vector
 CC system for production of NTR-5 is claimed. NTR-5 polypeptides can
 CC be used as immunogens and in screening assays to identify NTR-5
 CC ligands, agonists and antagonists. Polypeptides comprising the
 CC extracellular domain of NTR-5 fused to an immunoglobulin constant
 CC region, especially to a human immunoglobulin gamma-1 Fc region,
 CC are claimed. The invention also provides for diagnostic and
 CC therapeutic methods based on the interaction of NTR-5 and agents
 CC that initiate signal transduction through binding to NTR-5.

XX Sequence 328 AA;

Query Match 67.7%; Score 1544.5; DB 20; Length 328;
 Best Local Similarity 90.2%; Pred. No. 4.5e-134;
 Matches 286; Conservative 4; Mismatches 14; Indels 13; Gaps 3;

QY 1 MALKVLEQEKTEFTLLVLLGYLSCKVTCETGDCRQOEPRDRSGNVCVPCNQCGPWELSK 60
 DB 1 malkvleqektftllvllgylsckvtcesgdcrgqefdrsgnvcvpcnqcgpgmelsk 60
 QY 61 ECGFGYGEDAQCVTCRLHREKEDWGFKCKPCLDCAVNNRFQKANGSATSDAICGDCPLG 120
 DB 61 ecgfygedaqvctrlhrfkedwgfkckpeldcavnnrfqkangsatsdaicgdcplg 120
 QY 121 FYRKTLLVGFQDMCEVPCGDPDPPEPHCAKSKVNLVKIASTASPRDTALAAVICSALAT 180
 DB 121 fyrktllvlgfmdmcevpchgdpdppephcaskvnlvkiastasprdtalaavicsalat 180
 QY 181 VLLALILCVIYCKRQFMKKPSWLSRSDIOYNGSELSCLDRPOLHEYAHRAACCCRRD 240
 DB 181 vllalilcvlyckrgfmekppswlsrsdiongselscldrpolheyaahracccrrd 240
 QY 241 SVQTGCVRLPLSMCCBEACSPNATLGGCVHSAASLQARNAGPAGEMVPTFFGSLTQSI 300
 DB 241 svqtgcvrllpsmcceacspnatlggcvhsaaslqarnagpagemvptffgsltsqi 300
 QY 301 CGEFSQDAPLQMPMG 317
 DB 294 c-----wnpkstpllg 304

RESULT 8
 Y06522
 ID Y06522 standard; Protein; 214 AA.

XX Y06522;
 XX Y06522;
 DT 08-OCT-1999 (first entry)

XX Mouse STRIFE1 (Tango 127a) TNF receptor.

DE STRIFE1; Tango 127a; mouse; tumour necrosis factor receptor;
 KW sepsis; circulatory collapse; toxic shock; infection;
 KW immune disease; autoimmune disease; alcohol-induced hepatitis;
 KW inflammation; graft versus host pathology; cancer; tumour;
 KW cerebral malaria; multiple sclerosis; diagnosis; therapy.

XX Mus musculus.

XX Key Location/Qualifiers
 FT Peptide 1..29
 FT /note= "signal peptide" 30..214
 FT Protein /note= "mature protein" 34..72
 FT Domain /note= "cysteine-rich domain" 75..114
 FT Domain /note= "cysteine-rich domain"

FT Domain 169..193
 FT /note= "transmembrane domain"
 XX
 XX WO9937818-A1.
 XX PN
 XX 29-JUL-1999.
 XX PD
 XX 27-JAN-1999; 99WO-US01679.
 XX PF
 XX 27-JAN-1998; 98US-0014195.
 XX PR
 XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 XX PA
 XX Busfield SJ;
 XX PI
 XX WPI; 1999-458707/38.
 XX DR N-PSDB; X87394.
 XX
 XX New STRIFE1 and STRIFEII polypeptides, proteins and nucleic acid
 XX molecules useful for modulating TNFR associated disorders
 XX
 XX Claim 26; Fig 1A-B; 119pp; English.
 XX
 XX The present sequence represents mouse STRIFE1 (also called Tango
 CC 127a or T127a), a novel member of the tumour necrosis factor
 CC receptor (TNFR) superfamily. 2 Splice forms of murine STRIFE have
 CC been identified, one that is predicted to be membrane-bound
 CC (STRIFE1) and one that is secreted (STRIFE2, see Y06523). STRIFE
 CC was identified as a TNFR homologue by a computer-based search of
 CC EST databases. The invention provides STRIFE1 and STRIFE2
 CC polynucleotides and polypeptides, fusion proteins, antigenic
 CC peptides and antibodies. It also provides expression vectors,
 CC host cells and transgenic animals, as well as diagnostic, screening
 CC and therapeutic methods. STRIFE I and STRIFE II may play a role in
 CC mediating inflammatory, immune and host defense functions and may
 CC play a role in various neoplastic disease states. They may be
 CC useful as targets for developing novel diagnostic and therapeutic
 CC agents for TNF- and TNFR-associated disorders such as sepsis
 CC syndrome, circulatory collapse and shock resulting from bacterial
 CC infection, acute and chronic parasitic or infectious processes,
 CC acute and chronic immune and autoimmune pathologies, alcohol-induced
 CC hepatitis, chronic inflammatory pathologies, vascular inflammatory
 CC pathologies, graft-versus-host pathology, malignant pathologies
 CC involving TNF-secreting tumors, cerebral malaria and multiple
 CC sclerosis.
 XX
 XX Sequence 214 AA;

Query Match 42.8%; Score 977; DB 20; Length 214;
 Best Local Similarity 84.6%; Pred. No. 4e-82;
 Matches 176; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

QY 1 MALKVLEQEKTEFTLLVLLGYLSCKVTCETGDCRQOEPRDRSGNVCVPCNQCGPWELSK 60
 DB 1 malkvleqektftllvllgylsckvtcesgdcrgqefdrsgnvcvpcnqcgpgmelsk 60
 QY 61 ECGFGYGEDAQCVTCRLHREKEDWGFKCKPCLDCAVNNRFQKANGSATSDAICGDCPLG 120
 DB 61 ecgfygedaqvctrlhrfkedwgfkckpeldcavnnrfqkangsatsdaicgdcplg 120
 QY 121 FYRKTLLVGFQDMCEVPCGDPDPPEPHCAKSKVNLVKIASTASPRDTALAAVICSALAT 180
 DB 121 fyrktllvlgfmdmcevpchgdpdppephcaskvnlvkiastasprdtalaavicsalat 180
 QY 181 VLLALILCVIYCKRQFMKKPSWLSRSDIOYNGSELSCLDRPOLHEYAHRAACCCRRD 240
 DB 181 vllalilcvlyckrgfmekppswlsrsdiongselscldrpolheyaahracccrrd 240

RESULT 9
 W98145
 ID W98145 standard; Protein; 214 AA.

QY 61 ECGFGYGEDAQCVTCRLHFRKEDWGFKCKPCLDCAVAVNRFOKANGSATSDAICGDCPLG 120
 Db 61 ecgfygedaqcvpcprhrfkedwgfgkckpcadcalvnfrqncshsdavcgdcplg 120
 QY 121 FYRKTCLVGFQDMECVPCGDPDPPEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
 Db 121 fyrtkklvgfdmecnvpcgdpdppephctskvnlvkiastvssprdtalaavicsalat 180
 QY 181 VLLALLILCVIYCKRPFMEKKPSWSLRS 208
 Db 181 vllallilcvyckrfmekkpscklps 208
 RESULT 11
 Y22223
 ID Y22223 standard; Protein: 210 AA.
 AC Y22223;
 DT 16-SEP-1999 (first entry)
 DE Human TNFR superfamily soluble receptor protein sequence.
 XX TNFL1; human: TNFR superfamily: tumour necrosis factor ligand; TNF;
 KW tumour necrosis factor receptor; TNFR superfamily: cell proliferation;
 KW cell differentiation; cytokine production; immunoglobulin; hyperplasia;
 KW apoptosis inducer; activated T cell; autoimmune disease; inhibitor;
 KW myasthenia gravis; insulin-dependent diabetes mellitus; endotoxic shock;
 KW rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;
 KW tumour; proliferative disorder; neoplasia; dysplasia; immunocompetence;
 KW lymphoid organogenesis; bacterial resistance; contact hypersensitivity;
 KW delayed type sensitivity; therapy.
 XX Homo sapiens.
 OS
 XX
 PN W09933980-A2.
 XX
 PD 08-JUL-1999.
 XX
 PF 22-DEC-1998; 98WO-US27474.
 XX
 PR 16-DEC-1998; 98US-0212270.
 PR 30-DEC-1997; 97US-0068959.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Kassam A, Lamson G, Pot D, Tribouley C;
 XX
 DR WPI; 1999-405508/34.
 DR N-PSDB; X84622.
 XX
 PT New tumour necrosis factor ligands, useful for induction of cell
 XX death and/or proliferation of cells
 PS
 XX Claim 13; Page 62; 69pp; English.
 CC This sequence represents a tumour necrosis factor receptor (TNFR)
 CC superfamily soluble protein of the invention. The invention also relates
 CC to tumour necrosis factor (TNF) ligand (TNFL) family proteins. The TNFL
 CC proteins play regulatory roles in cell proliferation and/or
 CC differentiation, e.g. they can induce production of cytokines,
 CC immunoglobulins, etc. A variety of diseases can be treated by modulating
 CC the activity of TNFL proteins, e.g. they can induce apoptosis of
 CC activated T cells but rescue resting T cell from apoptosis. TNFL
 CC polypeptides can therefore be used to treat autoimmune diseases, such as
 CC myasthenia gravis, insulin-dependent diabetes mellitus, rheumatoid
 CC arthritis, multiple sclerosis, and systemic lupus erythematosus. TNFL
 CC proteins also have tumour stimulating properties, so tumours can be
 CC treated by inhibiting the expression or activity of TNFL. Other
 CC proliferative disorders, such as neoplasias, dysplasias, and hyperplasia
 CC can also be treated using TNFL inhibitors. The TNFL polypeptides and
 CC polynucleotides can also be used to enhance or decrease TNF activity,
 CC thus providing therapeutic benefits such as induction of cell death,

CC lymphoid organogenesis, or host bacterial resistance, and inhibition of
 CC endotoxic shock, contact hypersensitivity, delayed type sensitivity or
 CC immunocompetence of a transplant recipient. TNF and its receptors play a
 CC major role in host defence and immunosurveillance. As such, there is a
 CC need to identify new members of TNFR families. This invention provides
 CC this need.
 XX
 SQ Sequence 210 AA;
 Query Match 38.1%; Score 869; DB 20; Length 210;
 Best Local Similarity 83.7%; Pred. No. 3.4e-72;
 Matches 154; Conservative 11; Mismatches 19; Indels 0; Gaps 0;
 QY 1 MALKVLLLEQEKTFETLLVLLGLYSCKVTCTGTGDCRQERDRSGNCPNOCGPGMELSK 60
 Db 1 malkvlpbhrvtlfaallflhlaackvscetgdcrgqfkdrgnvcvickqcgpgmelsk 60
 QY 61 ECGFGYGEDAQCVTCRLHFRKEDWGFKCKPCLDCAVAVNRFOKANGSATSDAICGDCPLG 120
 Db 61 ecgfygedaqcvpcprhrfkedwgfgkckpcadcalvnfrqncshsdavcgdcplg 120
 QY 121 FYRKTCLVGFQDMECVPCGDPDPPEPHCASKVNLVKIASTASSPRDTALAAVICSALAT 180
 Db 121 fyrtkklvgfdmecnvpcgdpdppephctskvnlvkiastvssprdtavaavicsalat 180
 QY 181 VLLA 184
 Db 181 vlla 184
 RESULT 12
 W98148
 ID W98148 standard; Peptide: 150 AA.
 AC W98148;
 XX
 DT 05-JUL-1999 (first entry)
 XX
 DE TRAIN-R short, soluble form.
 XX
 KW TRAIN-R; receptor; human; tumour necrosis factor receptor;
 KW agonist; antagonist; cancer; immunological disease; therapy;
 KW cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN W09913078-Al.
 XX
 PD 18-MAR-1999.
 PF 11-SEP-1998; 98WO-US19030.
 XX
 PR 06-MAY-1998; 98US-0084422.
 PR 12-SEP-1997; 97US-0058631.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Hession C, Tschopp J;
 XX
 DR WPI; 1999-229238/19.
 XX
 PT New cysteine-rich tumor necrosis factor receptor
 XX
 PS Disclosure; Page 28; 30pp; English.
 CC The present sequence comprises the putative short, secreted soluble
 CC form of a novel human cysteine-rich tumour necrosis factor receptor
 CC family member termed TRAIN-R. The sequence was produced from a
 CC 30-amino acid peptide (see W98147) encoded by a cloned exon
 CC sequence (see X24979) and by comparison to the murine TRAIN-R
 CC short form (see W98144). The human soluble TRAIN-R protein is
 CC expected to inhibit signalling by full-length human TRAIN-R (see

CC W98146). Human TRAIN-R is expressed at low levels in every tissue
CC and cell line tested thus far, with higher expression detected in
CC heart, prostate, ovary, testis, peripheral blood lymphocytes,
CC thyroid and adrenal gland. Cell death can be induced by
CC administering an agent capable of inhibiting the binding of TRAIN-R
CC to its ligand. A claimed method of treating, or reducing, the
CC advancement, severity or effects of an immunological disease in a
CC mammal comprises administering a pharmaceutical composition which
CC comprises a TRAIN-R blocking agent, e.g. soluble TRAIN-R. TRAIN-R
CC can be fused to an immunoglobulin to produce a fusion protein which
CC may be targeted to various sites. It can be used in binding assays,
CC and to identify antagonists and agonists. Anti-TRAIN-R antibodies
CC can be used to reduce the severity of an immune response or to treat
CC cancer. TRAIN-R blocking agents can also be used to reduce the
CC severity or effects of an immunological disease (all claimed).

XX SQ Sequence 150 AA;

Query Match 37.4%; Score 854; DB 20; Length 150;
Best Local Similarity 99.3%; Pred. No. 5e-71;
Matches 148; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALKVLLDQKFTFLVLLGLYLSCKVTCETGDCRQQRDRSGNVCPCNCGPGMELSK 60
DB 1 malkvllleqektffllvllgylsckvtcesgdcrgqefdrsgncvpcnqpgmelsk 60
QY 61 ECGFGYGDAOCVTCRLHREFKEDWGFOCKPCLDCAVNVNRFQKNCATSATSDAICGLPG 120
DB 61 ecgfgyggedaqcvtcrhlrfkdwgfgkcpcldcavvnrfqkncatsatdaicgdlpg 120
QY 121 FYRKTGLVGFQDMCVPCGDPDPPEPHC 149
DB 121 fyrktglvgfdmccvpcgdpdppephc 149

RESULT 13

ID Y06399 standard; Protein; 160 AA.

XX AC Y06399;

XX DT 20-SEP-1999 (first entry)

XX DE Mouse NTR-5 receptor.

XX KW NTR-5; mouse; receptor; signal transduction; bone; muscle;
XX diagnosis; therapy.

XX OS Mus musculus.

XX PN W09933967-A2.

XX PD 08-JUL-1999.

XX PF 28-DEC-1998; 98WO-US27688.

XX PR 29-DEC-1997; 97US-0068925.

XX PA (REGE-) REGENERON PHARM INC.

XX PI Valenzuela DW;

XX DR WPI: 1999-419102/35.

XX DR N-FSDB; X59345.

XX PT New mammalian receptor NTR-5 polypeptides

XX PS Example 1; Page 19; 27pp; English.

XX CC The present sequence represents a novel murine receptor, designated
XX NTR-5, that shows homology to osteoprotegerin and to tumour necrosis
XX factor receptor. The sequence was predicted from isolated cDNA

CC clones (see X59345). Human NTR-5 has also been identified (see
CC Y06400). Homology to osteoprotegerin suggests that NTR-5 is
CC involved in the regulation of bone mass, and may be useful for
CC regulating development, proliferation and death of osteoblast or
CC osteoclast cells or for regulating muscle metabolism, and that it
CC may be implicated in muscle diseases or disorders. A host-vector
CC system for production of NTR-5 is claimed. NTR-5 polypeptides can
CC be used as immunogens and in screening assays to identify NTR-5
CC ligands, agonists and antagonists. The invention also provides for
CC diagnostic and therapeutic methods based on the interaction of
CC NTR-5 and agents that initiate signal transduction through binding
CC to NTR-5.

XX SQ Sequence 160 AA;

Query Match 34.3%; Score 783; DB 20; Length 160;
Best Local Similarity 91.6%; Pred. No. 1.9e-64;
Matches 141; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 55 GMELSKGCGYGGDAOCVTCRLHREFKEDWGFOCKPCLDCAVNVNRFQKNCATSATSDAIC 114
DB 1 gmelskcgfyggedagcvcprhfkdwgfgkcpcldcavvnrfqkncatsdavic 60

QY 115 GDCLPFGFYRKTGLVGFQDMCVPCGDPDPPEPHCASKVNLVKIASTASSPRDTALAAYI 174
DB 61 gdcldpgfyrktglvgfdmccvpcgdpdppephctskvnlvkisstvsprdtalaavi 120

QY 175 CSALATVLLALLILCVIYCKRQFMKPKPSWLSRS 208

DB 121 csalatvllallilcvlyckrqfmekpkpscklps 154

RESULT 14

ID Y06523 standard; Protein; 150 AA.

XX AC Y06523;

XX DT 08-OCT-1999 (first entry)

XX DE Mouse STRIFE2 (Tango 127b) TNF receptor.

XX KW STRIFE2; Tango 127b; mouse; tumour necrosis factor receptor;
XX sepsis; circulatory collapse; toxic shock; infection;
XX immune disease; autoimmune disease; alcohol-induced hepatitis;
XX inflammation; graft versus host pathology; cancer; tumour;
XX cerebral malaria; multiple sclerosis; diagnosis; therapy.

XX OS Mus musculus.

XX PH Key Location/Qualifiers

XX FT Peptide 1..29

XX FT /note= "signal peptide"

XX FT Protein 30..150

XX FT /note= "mature protein"

XX FT Domain 34..72

XX FT /note= "cysteine-rich domain"

XX FT Domain 75..114

XX FT /note= "cysteine-rich domain"

XX PN W09937818-A1.

XX PD 29-JUL-1999.

XX PF 27-JAN-1999; 99WO-US01679.

XX PR 27-JAN-1998; 98US-0014195.

XX PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX PI Busfield SJ;

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OM protein - protein search, using sw model

Run on: February 16, 2001, 21:05:27 ; Search time 20.9 seconds
(without alignments)
363.437 Million cell updates/sec

Title: US-09-380-276A-8
Perfect score: 2283
Sequence: 1 MALKVLLLEQKFTFTLLVLL.....AIHPATQTSLOWRRLGSL 423

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

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3: /cgn2_6/ptodata/2/iaa/6_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/PTCUS_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	159	7.0	438	1	US-08-097-827-11
2	159	7.0	438	1	US-08-494-574-11
3	150	6.6	206	1	US-08-097-827-7
4	150	6.6	206	1	US-08-494-574-7
5	145	6.4	205	3	US-08-974-022-51
6	144	6.3	1104	2	US-08-327-832-5
7	144	6.3	1104	2	US-08-828-584-5
8	136	6.0	625	3	US-08-996-139-15
9	134	5.9	186	1	US-08-089-458B-6
10	133.5	5.8	2050	2	US-08-347-594A-2
11	132.5	5.8	197	2	US-08-505-606-1
12	131	5.7	139	2	US-08-219-237B-8
13	129	5.7	326	1	US-08-292-549-4
14	129	5.7	326	1	PCT-US91-02207-4
15	128.5	5.6	1170	1	US-08-313-288B-20
16	128	5.6	355	1	US-08-292-549-6
17	124.5	5.5	1111	1	US-08-317-450B-15
18	124.5	5.5	1111	3	US-08-800-593-15
19	124.5	5.5	1193	1	US-08-317-450B-13
20	124.5	5.5	1193	3	US-08-800-593-13
21	124.5	5.5	2813	3	US-08-896-449A-2
22	124.5	5.5	2813	3	US-09-132-652-2
23	123.5	5.4	1171	1	US-08-445-135-1
24	123.5	5.4	3075	2	US-08-460-309-5
25	123.5	5.4	3075	2	US-08-125-077-5
26	121.5	5.3	311	3	US-08-911-423-8
27	120	5.3	256	1	US-08-236-918A-6
28	120	5.3	256	4	PCT-US96-03965-2

29 117.5 5.1 1251 4 PCT-US95-02251-3 Sequence 3, Appli
30 117.5 5.1 1252 1 US-08-199-780-3 Sequence 3, Appli
31 117.5 5.1 1252 2 US-08-316-650-3 Sequence 3, Appli
32 117 5.1 255 1 US-08-236-918A-8 Sequence 8, Appli
33 117 5.1 255 2 US-08-816-605-9 Sequence 9, Appli
34 117 5.1 255 4 PCT-US96-03965-8 Sequence 8, Appli
35 116 5.1 417 3 US-08-815-469-4 Sequence 2, Appli
36 116 5.1 428 3 US-08-815-469-2 Sequence 4, Appli
37 116 5.1 1010 3 US-08-882-046-7 Sequence 7, Appli
38 116 5.1 1218 2 US-08-400-159-6 Sequence 6, Appli
39 116 5.1 1218 3 US-08-611-729A-6 Sequence 6, Appli
40 116 5.1 1218 3 US-08-882-046-2 Sequence 2, Appli
41 114.5 5.0 1253 3 US-08-479-722B-4 Sequence 4, Appli
42 114 5.0 280 3 US-08-974-022-46 Sequence 46, Appli
43 114 5.0 455 1 US-08-050-319B-25 Sequence 25, Appli
44 114 5.0 455 1 US-08-321-668-2 Sequence 2, Appli
45 114 5.0 455 1 US-08-837-941-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-097-827-11
; Sequence 11, Application US/08097827
; Patent No. 5457035
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5457035el Cytokine which is a Ligand for
; TITLE OF INVENTION: OX40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/097.827
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-097-827-11

Query Match 7.0%; Score 159; DB 1; Length 438;
Best Local Similarity 27.5%; Pred. No. 8.2e-07;
Matches 69; Conservative 31; Mismatches 93; Indels 58; Gaps 18;

QY 15 TLLVLLGVLSCVKTCTGCRQCFEDRSNG-CVFCNCGPGMELSKCGCGYGEDAQC 73

DB 9 TALLLLG-LTLGTVLRRLNCKVHTY--PSGHKC--CRCQPGHGMVNR--DHTRTLLCH 61

Db	62	PCETGTFNEAVNYDTCQKQCQCNHRSGSELUKQNCPTPQDITVC--RCRPGTQPR-----QD 114
Qy	133	-----MECVPCGDPpppyep-----HCASKVNVLKIASTASSPRDTALAAVIC---SALA 179
Db	115	SGYKLGVDYVCPC--PPGHFSPGNQACKPWTNCTLSGKQTRHPASDSDLV-CEDRSLLA 171
Qy	180	TVLIALLILCYICKROFMKKPSW-----SLRSDIOIYNGSELSCLDRPQLUHEYAHRACQ 236
Db	172	TLL-----WETQRTFRFTTVQSTTVMPRTSELP--STPTLVE--PRSC-- 211
Qy	237	CRDSDVQTCGP 247
Db	212	---DKTHTCpP 219

RESULT 3
 US-08-097-827-7
 ; Sequence 7, Application US/08097827
 ; Patent No. 5457035
 ; GENERAL INFORMATION:
 ; APPLICANT: Baum, Peter
 ; APPLICANT: Goodwin, Ray
 ; APPLICANT: Fanslow, William
 ; APPLICANT: Gayle, Richard
 ; TITLE OF INVENTION: No. 5457035el Cytokine Which is a Ligand for
 ; TITLE OF INVENTION: OX40
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/097,827
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Perkins, Patricia A.
 ; REGISTRATION NUMBER: 34,693
 ; REFERENCE/DOCKET NUMBER: 2806
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 206-587-0730
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 206 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-097-827-7

```

Query Match      6.6%; Score 150; DB 1; Length 206;
Best Local Similarity 30.1%; Pred. No. 2e+06;
Matches 55; Conservative 21; Mismatches 75; Indels 32; Gaps 13;

QY 15 TLLVLLGYLSCKVTCETGDCRQOEFRRBSGN-CVPCNOCGPGMELSKECGFYGEDAOCV 73
      ||||| || : : : : || : : || : : || : : || : : || : : || : : ||
Db 9 TALLLLG-LTIGVTFARRLNCVKHTY--PSGHKC--CRECQFGHGMVNRK--DHTRDTLCH 61
      || : : || : : || : : || : : || : : || : : || : : || : : ||

QY 74 TCRLHREKEDMGFOKPCPLCDCAVVNRFO-KANGSAYSDAICGOCPLCFYRKTLLVGPOD 132
      || : : || : : || : : || : : || : : || : : || : : || : : ||
Db 62 PCETGFGFNEAVNYDTCKOCTOCNHRSSSELKQNTPTQDQTV-CRCRGTQPR-----QD 114
      || : : || : : || : : || : : || : : || : : || : : || : : ||

QY 133 -----MECVPCGDDPPPPYEP-----HCASKVNLVKIIASTASPRDTLAAVVC---SALA 179
      ||||| || : : : : || : : || : : || : : || : : || : : || : : ||
Db 115 SGYGLGVDCVPC---PPGHFSPGNNOACKPWTNCTLSGKOTRIPASDSLDVAY-CEDRSLLA 171
      || : : || : : || : : || : : || : : || : : || : : || : : ||

```


; TITLE OF INVENTION: Retroviral Expression Constructs Thereof
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Banner, Birch, McKie & Beckett
 ; STREET: 1001 G Street, N.W.
 ; CITY: Washington, D.C.
 ; STATE: District of Columbia
 ; COUNTRY: U.S.A.
 ; ZIP: 20001
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/327,832
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Posorske, Laurence H.
 ; REGISTRATION NUMBER: 34,698
 ; REFERENCE/DOCKET NUMBER: 1107.46362
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 20-2 508-9153
 ; TELEFAX: 202 508-9299
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1104 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-327-832-5

Query Match 6.3%; Score 144; DB 2; Length 1104;
 Best Local Similarity 18.8%; Pred. No. 7.4e-05;
 Matches 110; Conservative 59; Mismatches 181; Indels 236; Gaps 27;
 QY 24 SKVTCETGDCRQEFDRSGNVCPCNCGPGMELSKGCG-----FCYGEDAQC-----72
 Db 440 SCNLLCHPG-----PCPPCPAFMTKCEGRTHTVRCQAVSVHCSNPC 484
 QY 73 ---VTCRLHRFKEDWGQKCKPCLDCAVVNRQKANCATS-DAICGDCPLPGFYRKTCLV 128
 Db 485 ENILNCGQHCAELCHGGCQPCQ---IILN--QVCYCGSTSRDLVCGTDV-----GKSD 534
 QY 129 GFQDMEC-----VPCGD-----PPH-----PYEPHC--ASKVNLVKIASTASS 164
 Db 535 GFGDFSLCTCKGDKLCKGNHTCSQVCHPQCCQCPRLPOLVRCPCGQTPLSQLELGS 594
 QY 165 PRDIALAAV-----IC-SALATVLLALLILC-----VIYKROFMEKK- 201
 Db 595 SRKTCMDPVPSCGKVCCKPLPGSLDFIHTCEKLCHEGDCGVPVSRVTSVSCRSFRTKEL 654
 QY 202 PWSLSRSDI-----QYNGSELCLDRPQ-----LH-----EYA 230
 Db 655 PCTSLKSEDATEMCDKRCNKRKLCGRHKNCICCCVDKHKHKLNCGRKLCRGLHRCCEPC 714
 QY 231 HRACCO-CRRDSVQT-----CGPVLPLSMCC-----BE 258
 Db 715 HRNGCQTQWASFDLTCCHGASVIYPPVPCGTRPCTQTCARVHECDHPVYHSHSE 774
 QY 259 ACS-----PNPATLGGCVHSAASL-----277
 Db 775 KCPPTFTLQKCMGKHEFRSNIPCHLVDSICGLPCSATLPCGMHKCQRLCHKHGLVDE 834
 QY 278 -----QAR-----NAPGAGEMVPTFFGSLTQSI 300
 Db 835 PKQPCTTPRADCGHPCMAPCHTSSPCPVTAACKAKVELCEGCRKEMVICSEASSTYQR 894
 QY 301 CGEFSDAWPLMQNPGDDNISCDSPYELTGEDIHSLNPELESSTSLDSSNQDLVGGAV 360
 Db 895 IAAISMASKITDQMLGGS-----VEISKLTITKKEVHOARLECEDECSALERKKR--LAFAF 948

QY 361 PVQSHSENAATDLRSYNNITLVESATQDALTMRSQLDQSGAIL 406
 Db 949 HISESDPENIRSSGSKFSDSLKEDA--RKDLKFVSDVEKEMETLV 992
 RESULT 7
 US-08-828-584-5
 ; Sequence 5, Application US/08828584
 ; Patent No. 5908762
 ; GENERAL INFORMATION:
 ; APPLICANT: Ono, Santa J.
 ; APPLICANT: Strominger, Jack L.
 ; TITLE OF INVENTION: Transcription Factor Regulating MHC
 ; EXPRESSION, CDNA and Genomic Clones Encoding Same and
 ; TITLE OF INVENTION: Retroviral Expression Constructs Thereof
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Banner, Birch, McKie & Beckett
 ; STREET: 1001 G Street, N.W.
 ; CITY: Washington, D.C.
 ; STATE: District of Columbia
 ; COUNTRY: U.S.A.
 ; ZIP: 20001
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/828,584
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Posorske, Laurence H.
 ; REGISTRATION NUMBER: 34,698
 ; REFERENCE/DOCKET NUMBER: 1107.46362
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 20-2 508-9153
 ; TELEFAX: 202 508-9299
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1104 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-828-584-5

Query Match 6.3%; Score 144; DB 2; Length 1104;
 Best Local Similarity 18.8%; Pred. No. 7.4e-05;
 Matches 110; Conservative 59; Mismatches 181; Indels 236; Gaps 27;
 QY 24 SKVTCETGDCRQEFDRSGNVCPCNCGPGMELSKGCG-----FCYGEDAQC-----72
 Db 440 SCNLLCHPG-----PCPPCPAFMTKCEGRTHTVRCQAVSVHCSNPC 484
 QY 73 ---VTCRLHRFKEDWGQKCKPCLDCAVVNRQKANCATS-DAICGDCPLPGFYRKTCLV 128
 Db 485 ENILNCGQHCAELCHGGCQPCQ---IILN--QVCYCGSTSRDLVCGTDV-----GKSD 534
 QY 129 GFQDMEC-----VPCGD-----PPH-----PYEPHC--ASKVNLVKIASTASS 164
 Db 535 GFGDFSLCTCKGDKLCKGNHTCSQVCHPQCCQCPRLPOLVRCPCGQTPLSQLELGS 594
 QY 165 PRDIALAAV-----IC-SALATVLLALLILC-----VIYKROFMEKK- 201
 Db 595 SRKTCMDPVPSCGKVCCKPLPGSLDFIHTCEKLCHEGDCGVPVSRVTSVSCRSFRTKEL 654
 QY 202 PWSLSRSDI-----QYNGSELCLDRPQ-----LH-----EYA 230
 Db 655 PCTSLKSEDATEMCDKRCNKRKLCGRHKNCICCCVDKHKHKLNCGRKLCRGLHRCCEPC 714

```

QY      231 HRACCO--CRDVSQT-----CGPVRLLPSMCC-----EE 250
       !!   !! : !     !! : ! : ! : !         |||          || 
Db      715 HRCNCOTCWOASDELTCGASVIYPVPCGTPTCTCARVECDHPVYHSGHSEE 774
       !!           !!               !!             |!|||!!    |
QY      259 ACS-              -PNPATLGGCVHSAA$SL----- 277
       |                |!!!!!!!|!|            |
Db      775 KCPCTFLTKWCMKGHEFRSNTPCHLVLDISCLGPCSATLPGMHHKQRCLCHKGECLVDE 834
       |                |!!!!!!!!!!!!!!!!OAR-----NAGPAGEVMPTFFGSILTQSI 300
QY      278 -----PKOPCTTTRADCGHCPCMAPCHTSPPVTACKAKVELQCCEGRRKEMVICSEASSTYOR 894
       |                |:::||:|||||
Db      835 PKOPCTTTRADCGHCPCMAPCHTSPPVTACKAKVELQCCEGRRKEMVICSEASSTYOR 894
       |                |:::||:|||||
QY      301 CGFESDAWLPMQNMGDDNISFCDSYPELTGEDIH$NLNPBELSSITSDSNSODLVGGAV 360
       !!           !!!        ::!:!!!!!!|:|:|:~::~|
Db      895 IAI$MSASKITDMQLQS-----VEISKLTIKKEHVHORLEDCEDCSALERKKR--LAEAF 948
       !!           !!!        ::!:!!!!!!|:|:|:~::~|
QY      361 PVOSHENFTAATDLGRYNNTLVESA$TDALTMRSOLDQESAILI 406
       | : ! : ~::::|:|:|:|:|:|:~::::|
Db      949 HI$EDSDPFNIIRSGSKFSDSLAKEDA--RKDKLFVDVEKETMETIV 992
       | : ! : ~::::|:|:|:|:|:|:~::::|

RESULT      8
US-08-996-139-15
; Sequence 15, Application US/08996139
; Patent No. 6017729
GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 625 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-996-139-15
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Query Match 6.0%; Score 136; DB 3; Length 625;

```

Best Local Similarity 22.2%; Pred. No. 0.00019;
Matches 102; Conservative 51; Mismatches 171; Indels 136; Gaps 27;

QY 16 LLVLVLGSLCKVTCE-TGDCRQOEFRDRSGNCVPCNOCGPGMELSKGEGVGEDAOCVT 74
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 18 LCVLL--VPLQVTLQVTPCQERHYEHLGR--CSRCEPKYLSSKC--TPTSDSVCLP 71
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 75 CRLHFRKEDMGQ-KC---KPC-LDCAVV-----NRFOKANC SAT-----SDAIC---- 114
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 72 CGPDEYLDTWNEEDKLLHKVCDAGKALVAVDPGNHTAPRRCACTAGYHWNSDCECCRRN 131
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 115 GDCLPGRYRKTLLGVQDMCEVPC-----GDPPPPY-----EPH----- 148
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 132 TECAPGCGAOPHLQNKDVTCTCLLGPFFSDVFSSTDKCKPWNCTLLGLKLEAHOGTTES 191
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 149 --CASKVNLVKIASTASSPRDTALAAVICSALATVLLALLTLCVYCKRFMEKKPSWS 205
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 192 DVGCSSTM LRRPKEAQYIPLSL--VLLFISVVVVAALIFGVYKKGKALTANLWN 249
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 206 -LRSQDIQYNGSELSCDLRDPOLHEYHARCC---QCRDRSVQTCGPVRLLPSMCEEACS 261
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 250 WNDACSSLGKNKSSGDR-----CAGSHSATSSQOCEVCB GILL--MTREKMW 296
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 262 PNPATLGGCVISAAS-----LQARNAGAPAGVPT-----FTGS 295
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 297 PEDGAGVCGPYCAAGGPWAERYDRSRTFTLVSEVETQGLSRKIPTDEYTD RPSQPTGS 356
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 296 LTQSTCGFEFSDAWPLMQNPM---GGDNLISFC-----DSYP ELT 330
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 357 LL--LIQOGSKSIPIPFQEPLEVGENDSLSCQFTGTSTVDSGCDFTBPPSR TDSMP--V 412
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 331 GEDIHSLNPELESSTSL-----DSNSSQDLVG-GAVPVQSH 365
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 413 SPEKH-LTKEIEGDSLCPWVYSSNSTDGYTSGNTPGEDH 451
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
US-08-089-458B-6
; Sequence 6, Application US/08089458B
; Patent No. 5359039
; GENERAL INFORMATION:
; APPLICANT: Smith, Craig
; APPLICANT: Goodwin, Raymond
; TITLE OF INVENTION: Isolated Poxvirus A53R-Equivalent Tumor
; TITLE OF INVENTION: Necrosis Factor Antagonists
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patricia Anne Perkins, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word, Version #5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/089, 458B
; FILING DATE: 07/09/93
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 186 amino acids

```


Db 59 HRSSELKONCPTEDTVC--QCRPGTQPRODSHHKLGVDVCPC--PGCHFSPGSGNOACKP 115

11;

RESULT 13
US-08-292-549-4
; Sequence 4, Application US/08292549
; Patent No. 5464938
; GENERAL INFORMATION:
; APPLICANT: Smith, Craig A.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Isolated Viral Protein TNF Antagonists
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101

/ COUNTRY: USA
 / STATE: Washington
 / CITY: Seattle
 / ZIP: 98101
 /
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patent In Release #1.0
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/292,549

CLASSIFICATION: 330
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/963,330
FILING DATE: 10/19/92
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2602-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 326 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-292-549-4

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-292-549-4

Query Match          5.7%  Score 129; DB 1; Length 326;
Best Local Similarity 24.1%  Pred. No. 0.00034;
Matches 49; Conservative 82; Indels 52; Gaps 12;

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Qy	123	-----RRTKL-VGF-----QDMCEVCGDPPPY-----EPHCASKNVLV	156
Db	116	QGEGRICAPKTKCPAGYGVSGHRTGDVLCTKC---PRYTSDAVSTETCTTSFNVI	171
Qy	157	KIATASSPRDTALAAVICSALA	179
Db	172	SVEENLYPVNDTS-----CTTTA	189

```

RESULT 15
US-08-313-288B-20
; Sequence 20, Application US/08313288B
; Patent No. 5750502
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M. and Avihu Klar
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas

```

Query Match 5.6%; Score 128.5; DB 1; Length 1170;
Best Local Similarity 21.1%; Pred. No. 0.0022;
Matches 87: Conservative 40; Mismatches 147: Indels 139;

Search completed: February 16, 2001, 21:05:30
Job time: 150 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 16, 2001, 21:06:39 ; Search time 31.47 Seconds
(without alignments)
912.678 Million cell updates/sec

Title: US-09-380-276a-8
Perfect score: 2283
Sequence: 1 MALKVLEQEKFTFTLLVLL.....AIHPATQTSLOVQRQLGSL 423

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_66:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	157	6.9	454	1 QOMST1	tumor necrosis fac
2	157	6.9	454	2 157826	tumor necrosis fac
3	147	6.4	416	1 JN0006	nerve growth facto
4	147	6.4	1797	2 A55677	laminin beta-2 cha
5	146.5	6.4	1801	1 MMRIS	laminin beta-2 cha
6	145.5	6.4	435	2 I54182	tumor necrosis fac
7	145	6.4	271	2 S12783	OX40 antigen precu
8	144	6.3	272	2 I48700	gene ox40 protein
9	144	6.3	1104	2 I38869	transcription fact
10	141.5	6.2	461	1 GQRT11	tumor necrosis fac
11	140	6.1	425	1 A26431	nerve growth facto
12	134	5.9	1786	1 MMSB1	laminin beta-1 cha
13	133.5	5.8	2813	1 VWHU	von Willebrand fac
14	132.5	5.8	1170	2 A40558	thrombospondin 1 p
15	132	5.8	277	2 A60771	B-cell activation
16	130	5.7	1798	2 S53869	laminin beta-2 cha
17	129	5.7	326	1 GQVZML	t2 protein - myxom
18	128.5	5.6	1170	1 TSHUP1	thrombospondin 1 p
19	127	5.6	1650	2 S53457	dominant autoantig
20	127	5.6	1827	2 T34288	hypothetical prote
21	127	5.6	4660	2 T42737	gp330 protein prec
22	125.5	5.5	1548	2 S34583	serine proteinase
23	124.5	5.5	1111	2 B44018	laminin B2t chain
24	124.5	5.5	1193	2 A44018	laminin B2t chain
25	124.5	5.5	3712	2 S18253	laminin alpha-1 ch
26	124	5.4	349	2 D72175	G2R protein - vari
27	123	5.4	837	2 S43656	furin (EC 3.4.21.7
28	122.5	5.4	1680	2 A43434	furin (EC 3.4.21.7
29	122	5.3	1299	2 T43231	furin (EC 3.4.21.7

ALIGNMENTS

RESULT 1

QOMST1

tumor necrosis factor receptor 1 precursor - mouse
N:Alternate names: tumor necrosis factor receptor, 55K
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence.revision 30-Jun-1992 #text_change 22-Jun-1999
C:Accession: A38634; B40254; S16677; S19021; I54532
R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto
A:Reference number: A38634; MUID:91187885
A:Accession: A38634
A:Molecule type: mRNA
A:Residues: 1-454 <LEW>
A:Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J Mol. Cell. Biol. 11, 3020-3026, 1991
A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f
A:Reference number: A40254; MUID:91246168
A:Accession: B40254
A:Molecule type: mRNA
A:Residues: 1-454 <G02>
A:Cross-references: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826
R:Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissoneghis, A.M.; Gray, P.W.; Fel Eur. J. Immunol. 21, 1649-1656, 1991
A:Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necro
A:Reference number: S16677; MUID:91285014
A:Accession: S16677
A:Molecule type: mRNA
A:Residues: 1-454 <BAR>
A:Cross-references: EMBL:X59238; NID:g53578; PIDN:CAA41922.1; PID:g53579
R:Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W. Immunogenetics 34, 338-340, 1991
A:Title: Molecular cloning and expression of the mouse Tnf receptor type b.
A:Reference number: S19021; MUID:92039815
A:Accession: S19021
A:Molecule type: mRNA
A:Residues: 1-454 <ROT>
A:Cross-references: EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849
R:Bebo, B.F. Immunogenetics 39, 450-451, 1994
A:Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cel
A:Reference number: I54532; MUID:94245292
A:Accession: I54532
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-454 <RES>
A:Cross-references: GB:I26349; NID:g430732; PIDN:AAA59361.1; PID:g430733
C:Comment: This protein is one of two distantly related receptors for both TNF-alpha
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>

gene G4R protein -
laminin gamma 2 ch
notch4 - mouse
membrane glycoprot
hypothetical prote
t-cell antigen 4-1
hypothetical prote
laminin beta-1 cha
VLDL receptor prec
latent transformin
laminin alpha-1 ch
4-1BB - human
lymphocyte activat
gene shuttle craft
laminin beta-1 cha
hypothetical prote

QY 34 CRQEFDRSGNCVPCNQCPCGMELSKCEGFCYGEDAQCVTCLRLHRPKEDNCF-QXKPC 92

```
F;262-416/Domain: Intracellular #status predicted <INT>
```

OV 20 LGYLSCKVTCETGD-----CROOEFDR-SGNCVPCNOCGPGMELSKCEGFGY-----G 67

```
Db 82 VGLHSMAPCVESDDAVRCAYGYFQDELGSCKECSIC-----EVGFLMFPGRDS 133
Qy 68 EDAQCVTCLRHREFEDWGFQKCKPCLDCAVV--NRFORANGSATSADCGCLPCFYRKT 125
Db 134 QDTVEECPEGTSEANF--VDPCLPCTICEENVMVWKECTASDAECRDLDHPRWTHHT 191
Qy 126 -KLGVFQDMECVPGDPPPPYEPHCASKVNLKIASTASSP---RDTA--LAAAVICSALA 179
Db 192 PSLAGSDSPE--PITRDPFNTGEMATTIADIVTTVMGSSQPVWSRGTDADNLIPYVCSILA 249
Qy 180 TVLLIALL 186
Db 250 AVVGLV 256

RESULT 4
A5677
laminin beta-2 chain precursor (version 1) - human
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 17-Mar-1999
C:Accession: A5677
R:Wewer, U.M.; Gerecke, D.R.; Durkin, M.E.; Kurtz, K.S.; Mattei, M.G.; Champliaud, M.F.;
Genomics 24, 243-252, 1994
A:Title: Human beta2 chain of laminin (formerly S chain): cDNA cloning, chromosomal loca
A:Reference number: A5677; MUID:95213013
A:Accession: A5677
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1797 <NEW>
A:Cross-references: GB:X79683
C:Genetics:
A:Gene: GDB:LAMB2
A:Cross-references: GDB:L32363; OMIM:150325
A:Map position: 3p21.3-3p21.2
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C:Keywords: basement membrane; extracellular matrix; glycoprotein; heterotrimer
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-1797/Product: laminin beta-2 chain #status predicted <MAT>
F:283-344/Domain: laminin-type EGF-like homology <LE01>
F:347-407/Domain: laminin-type EGF-like homology <LE02>
F:470-467/Domain: laminin-type EGF-like homology <LE03>
F:470-519/Domain: laminin-type EGF-like homology <LE04>
F:522-552/Domain: laminin-type EGF-like homology #status atypical <LE05>
F:783-828/Domain: laminin-type EGF-like homology <LE06>
F:831-874/Domain: laminin-type EGF-like homology <LE07>
F:877-924/Domain: laminin-type EGF-like homology <LE08>
F:927-982/Domain: laminin-type EGF-like homology <LE09>
F:985-1034/Domain: laminin-type EGF-like homology <LE10>
F:1037-1091/Domain: laminin-type EGF-like homology <LE11>
F:1094-1139/Domain: laminin-type EGF-like homology <LE12>
F:1142-1186/Domain: laminin-type EGF-like homology <LE13>

Query Match 6.4%; Score 147; DB 2; Length 1797;
Best Local Similarity 22.4%; Pred. No. 0.0053;
Matches 88; Conservative 35; Mismatches 144; Indels 126; Gaps 24;

Qy 17 LVLLGLSKVTCETGDCRQOEFRDRSGNCV-----PCNQCQPGMELSKCEGFGYG- 67
Db 775 LIYNGALPCQ---CNPOGSLSECNPHGQCLCKPGVWGRRCDCAPY-----YGFPG 825

Qy 68 -----EDAQCVTCLRLHFR-----KEDWGFQKCRKPCCL----- 93
Db 826 TCQACQCSPRGALLSLCERTSGQL-CEGTAFGLRCDACQRGQNGFFSCRCVCNGHAD 884
Qy 94 DCVAVNRFQKA--NC-SATSDAICGDCLPGFYRKTKLVGFQDMECVPCGDDP-PPYEPHC 149
Db 885 EC---NTHTGACLGCRDLTGGHEHCERCITAGPHGDRPLP--YGAQCRPCPCPBGPGSQRHF 939
Qy 150 ASKVNVLKIASTASSPRTALAAVICSALATVLLALLILCVLYCKRQFME-KKP----- 202
Db 940 AT-----SCHQDEYSQOIIVCHCRAGY---TGLRCEACAPGQFGDPSRPGACQLC 985
```

```
Qy 203 --SWSLRSDIQ-----YNGSELSCLE-----DRPOLHEYA-----HRACQCCRDS 241
Db 986 ECSGNIDPMDPADCPHGGQCLRLHHTGEPHCAHSKSGFGHQAARQSCHRCTCNLLGTN 1045
Qy 242 VQTC-----GPVRLPSM--CCEBACSPN--PATLGGCGVHSAASLQARNAGP- 284
Db 1046 PQQCPSPDQCHCDPSSGQCPCLPNVQALAVDRCAPFNWLTSGHGQCQPCACLPSEEGPT 1105
Qy 285 ----AGEMVP-TFFGSLTQSGSEFSDAWPLMQ 312
Db 1106 CNEFTGQCHPGAGFGGRTCSECELHWGDPGLQ 1138

RESULT 5
MARTS
laminin beta-2 chain precursor - rat
N:Alternate names: laminin chain B3; S-laminin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 10-Dec-1999
C:Accession: S03539
R:Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.
Nature 338, 229-234, 1989
A:Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the ne
A:Reference number: S03539; MUID:89159410
A:Accession: S03539
A:Molecule type: mRNA
A:Residues: 1-1801 <HUN>
A:Cross-references: EMBL:X16563; NID:g57250; PIDN:CAA34561.1; PID:g57251
C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type lamin
C:Function:
A:Description: interact with cells and with other basement membrane proteins to promo
C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellu
F:1-35/Domain: signal sequence #status predicted <SIG>
F:36-1801/Product: laminin beta-2 chain #status predicted <MAT>
F:36-285/Domain: VI <DOM6>
F:286-555/Domain: V <DOM5>
F:286-347/Domain: laminin-type EGF-like homology <LE01>
F:350-410/Domain: laminin-type EGF-like homology <LE02>
F:413-470/Domain: laminin-type EGF-like homology <LE03>
F:473-522/Domain: laminin-type EGF-like homology <LE04>
F:525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>
F:556-784/Domain: IV <DOM4>
F:786-831/Domain: laminin-type EGF-like homology <LE06>
F:788-1196/Domain: III <DOM3>
F:834-877/Domain: laminin-type EGF-like homology <LE07>
F:880-927/Domain: laminin-type EGF-like homology <LE08>
F:930-986/Domain: laminin-type EGF-like homology <LE09>
F:989-1038/Domain: laminin-type EGF-like homology <LE10>
F:1041-1095/Domain: laminin-type EGF-like homology <LE11>
F:1098-1143/Domain: laminin-type EGF-like homology <LE12>
F:1146-1190/Domain: laminin-type EGF-like homology <LE13>
F:1197-1412/Domain: II <DOM2>
F:1197-1412/Region: heptad repeats
F:1413-1445/Domain: alpha <ALP>
F:1446-1801/Region: heptad repeats
F:1446-1801/Domain: I <DOM1>
F:45-50/Disulfide bonds: #status predicted
F:251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #statu
F:1193,1196,1800/Disulfide bonds: interchain #status predicted

Query Match 6.4%; Score 146.5; DB 1; Length 1801;
Best Local Similarity 22.9%; Pred. No. 0.0057;
Matches 99; Conservative 33; Mismatches 146; Indels 155; Gaps 27;

Qy 17 LVLLGLSKVTCETGDCRQOEFRDRSGNCVPCNQCQPGMELSKCEC-----CFG--- 65
Db 778 LIYNGALPCQ---CDPQGSLSSECNPHGQCC-----RCKPGV-VGRRCACATGYGFGPAG 830
Qy 66 -----YGEDAQCVTCRLHFR-----KEDWGFQKCKPCLDCAVNVNR 101
```

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Db 831 CQACQCPDGAISALCEGTSGOCL-CRTGAFGLURCDHCQRGWGFNCRPC-----VCNG 884
QY 102 QKANCATSDAI-----CGDCLPGFYRKTKL-VGFQDMCEVPCGDDP-PPVEPH 148
Db 885 RADECDAGTACGLCRDYTGGEHCERCIAGFDGDLPLPGGQ---CRPCPCPGCSQRH 941
QY 149 CASKVNLVKTASTASSPRDTALAAVTSALATVLLALLILCVYKRPME-KKPSWSLR 207
Db 942 FAT-----SCHRDGYSQIVCHCRAGY---TGLRCEACAPGFCGDKSPKGGRCQ 987
QY 208 ----SQDIQ-----YNGSELSCLD-----RPLHEYA-----HRACCQCR 239
Db 988 LBCSGNIDPTDGACDPHTGQCLRLHHTGPHGCHCKPFGHCGAAROSCHRCTCNLLG 1047
QY 240 DSVOTC-----GPRVLLP---SMCCEACSPN--PATLGGCVHSAASLAARNA 282
Db 1048 TDQPCPSTDLCHCDPSTGOCPLPHVOGLSCDR-CAPFNWNTSGRCQPCACHFSRAR 1106
QY 283 GP-----AGEMVPTFFGSLTQSTCGEFSDAWPLMQ-----NPMGGD----- 318
Db 1107 GPTCNEFTGQCHCHAG-----EGGRTCEBQELHWGDPGLQCLACDCDPRGIDKPCQHR 1160
QY 319 NISFCDSPBLTG 331
Db 1161 STGHCSGCPGVSG 1173

RESULT 6
I54182
tumor necrosis factor receptor 2-related protein - human
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C:Accession: I54182
R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-219, 1993
A:Title: Construction and evaluation of a hncDNA library of human l2p transcribed sequen
A:Reference number: I54182; MUID:93252381
A:Accession: I54182
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-435 <RES>
A:Cross-references: GDB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
A:Gene: GDB:LTBR
A:Cross-references: GDB:L230195; OMIM:600979
A:Map position: 12p13.3-12p13.1
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 6.4%; Score 145.5; DB 2; Length 435;
Best Local Similarity 21.4%; Pred. No. 0.0014;
Matches 73; Conservative 41; Mismatches 108; Indels 119; Gaps 19;

QY 16 LVLVLGLYLSCK-----VTCETGDCRQGE---FRDRSGNVCVPCNCGGPGMELSKGCGFG 65
Db 18 VLGLGLLAASQPQAVPPYASENOTCRDQKEYEYEQHRIIC--CSRCPGTYVSARK--S 73
QY 66 YGEDAQCVTRLHRFRFEDMGF---QCKPC-----LDCAVVNRFOKANCATSADAIC- 114
Db 74 RIRDTVCATCAENSYNEHWNLYICQLCRPCDPMGLLEEIAPCTSKRKTCRCQCPQMFC 133
QY 115 -----GDCLPGFYRKTK-LVGFQDMCEVPC-----GDPpppPEPH--CAS 151
Db 134 AWALECTHCELLSDCPGTEAEKLDKDEGVGNHNCVCKAGHFQNTSSPASCQCPHTRCEN 193
QY 152 KVNVLVITA-----STASSPRD-----TALAAVICSALATVLLALLILCVIY---- 192
Db 194 Q-GLVEAAPGTAQSDTTCKNPLEPLPPENSGTMLMLAVLLPLAFFLLATVFCISWKSHP 252
QY 193 --CKR--QPMKKP-----SNLSRSDIYNGSELSCLDRPQLHEYAHRACCQCR 238
Db 253 SLCKRLGSLKRRQGGPNPVAGSW-----EPPKAHPYF----- 287
```

```
QY 239 RDSVQTCGPVRLLPSCMCCEACSPNPATLGGCVHSAASLQA 279
Db 288 PDLVQPLLPI-----SGDVSPVSTGLPAAVPLEA 316

RESULT 7
I52783
OX40 antigen precursor - rat
N:Alternate names: nerve growth factor receptor homolog
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C:Accession: I52783; S08036
R:Mallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphoc
A:Reference number: I52783; MUID:90214614
A:Accession: I52783
A:Molecule type: mRNA
A:Residues: 1-271 <MAL>
A:Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: growth factor receptor; transmembrane protein
F:1-15/Domain: signal sequence #status predicted <Sig>
F:20-271/Product: OX40 antigen #status predicted <MAT>
F:211-235/Domain: transmembrane #status predicted <TM>
```

```
Query Match 6.4%; Score 145; DB 2; Length 271;
Best Local Similarity 28.6%; Pred. No. 0.00094;
Matches 54; Conservative 23; Mismatches 76; Indels 36; Gaps 12;

QY 9 QEKTFETLLVLLGLYSCKVTCEGTGDCRQGEFRDR--SGN-CVPCNCGGPMELSKGCGFG 65
Db 6 QQTAFLLLGLSLGVTVKLC-----VKDTYPSGHKC--CRECQPGHGMVSR--D 52
QY 66 YGEDAQCVTRLHRFRFEDMGFQKRCPLCAVVRFPQ-KANCATSADAICDCLPGFYRK 124
Db 53 HTRDTVCHPCPCPGFYNEAVNYDFCKQCTQCNHRSGSELKQNTPTEDTV-C-QCRPGTQPR 111
QY 125 TKLVGFQDMCEVPCGDPpppPEP---HCASKVNLV---KIATASSPRDTALAIVC- 175
Db 112 QSSSHKGLGVDCVPC--PPGHFSPGSNQACKPWTNCTLSGKQIRHPASNSLDT-----VCE 164
QY 176 --SALATVL 182
Db 165 DRSLLATLL 173
```

```
RESULT 8
I48700
gene ox40 protein - mouse
N:Alternate names: OX40 antigen
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C:Accession: I48700; I48334; S34377
R:Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.
J. Immunol. 151, 5261-5271, 1993
A:Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell
A:Reference number: I48700; MUID:94044750
A:Accession: I48700
A>Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-272 <RES>
A:Cross-references: EMBL:X21674; NID:g312827; PIDN:CAA9772.1; PID:g312828
R:Birdland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX
A:Reference number: I48334; MUID:95255413
A:Accession: I48334
A>Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-14, 'G', 16-272 <RE2>
A:Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
```



```
QY 280 RNA-CPAG-----EMVPT-----FFGSL 296
      |||
      |.|||
      :|||
Db 303 SPVFGPSNMHNFVPPVREVPTQAGDPLLYGSL 335

RESULT 11
A26431
Nerve growth factor receptor precursor, low affinity - rat
N:Alternate names: NGF receptor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A26431; PH1229
R:Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
Nature 375, 593-597, 1987
A:Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
A:Reference number: A26431; MUID:87115859
A:Accession: A26431
A:Molecule type: mRNA
A:Residues: 1-425 <RAD>
R:Metzels, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.
Gene 121, 247-254, 1992
A:Title: Regulatory elements and transcriptional regulation by testosterone and retinoid
A:Reference number: PH1229; MUID:93077038
A:Accession: PH1229
A:Molecule type: DNA
A:Residues: 1-20 <MET>
A:Cross-references: GB:X61269
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of
C:Comment: This protein is thought to form a high-affinity receptor when it associates
C:Genetics:
A:Introns: 20/3
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-425/Product: nerve growth factor receptor #status predicted <MAT>
F:30-251/Domain: extracellular #status predicted <EXT>
F:33-66/Domain: NGF receptor repeat homology <NG1>
F:68-109/Domain: NGF receptor repeat homology <NG2>
F:110-148/Domain: NGF receptor repeat homology <NG3>
F:150-190/Domain: NGF receptor repeat homology <NG4>
F:198-249/Region: serine/threonine-rich
F:252-273/Domain: transmembrane #status predicted <MEM>
F:274-425/Domain: intracellular #status predicted <INT>
F:61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.1%; Score 140; DB 1; Length 425;
Best Local Similarity 20.8%; Pred. No. 0.0036;
Matches 85; Conservative 52; Mismatches 172; Indels 100; Gaps 20;

QY 16 LVLVLLYGLS--CKVTGTCGCRQOEFRDRSGNCVPCNQCQPGMELSKGCGYGEDAQCV 73
      ||:|||||
      ||:|||||
Db 18 LLLILVSSGGAKETCTG-----LYTHSGEC--CKACNLGEGVAQPCG---ANQTVCE 66

QY 74 TCRHREKED--WGFKCKPCLDCAVNVNFKANCATSDAICGDCPLGFKYRKT-----126
      |||
      |||
Db 67 PCLDNVTFSDVVSATEPCPKPCTECLGL-QSMSAPCVAEADAVC-RCAYGYQDEETGHCE 124

QY 127 -----LVGFQDMEVCPCGDPPEPPYEPHCASKVNLVKIATSPASSPRDTALAAVIC 175
      |||
      |||
Db 125 ACSVCEVSGSLVPSGCKQNTVCEECF---EGTYSDEAHV-----DPCLPCTVC 171

QY 176 SALATVLLALLILCVLYCKRQKFMKKPSLSRSDQIQNGSELSDLRDPOLHEHYAHRAC 235
      |||
      |||
Db 172 EDTERQLRE---CTPWADAECIEIPGRMIPRSTPTPEGSDSTAPSTQEPVPP-----220

QY 236 QCRDRSVQTCGPVRLPLPSMCCCEACSPNATLGGCGVHSAASLQARNAGPAGEMVPTFFGS 295
      |||
      |||
Db 221 --EQD-----LVPSTVADMVTT-----VMG-----SSQPVVTRGTTDLNLPVCSI 259
```


A:Description: interact with cells and with other basement membrane proteins to promote C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular F:1-21/Domain: signal sequence #status predicted <SIG> F:22-1786/Product: laminin beta-1 chain #status predicted <MAT> F:22-270/Domain: VI <DOM6> F:271-540/Domain: V <DOM5> F:271-332/Domain: laminin-type EGF-like homology <LE01> F:335-395/Domain: laminin-type EGF-like homology <LE02> F:398-455/Domain: laminin-type EGF-like homology <LE03> F:458-507/Domain: laminin-type EGF-like homology <LE04> F:510-540/Domain: laminin-type EGF-like homology #status atypical <LE05> F:541-772/Domain: IV <DOM4> F:773-1182/Domain: III <DOM3> F:773-818/Domain: laminin-type EGF-like homology <LE06> F:821-864/Domain: laminin-type EGF-like homology <LE07> F:867-914/Domain: laminin-type EGF-like homology <LE08> F:917-973/Domain: laminin-type EGF-like homology <LE09> F:976-1025/Domain: laminin-type EGF-like homology <LE10> F:1028-1081/Domain: laminin-type EGF-like homology <LE11> F:1084-1129/Domain: laminin-type EGF-like homology <LE12> F:1132-1176/Domain: laminin-type EGF-like homology <LE13> F:1183-1397/Domain: II <DOM2> F:1183-1397/Region: heptad repeats F:1398-1430/Domain: alpha <ALP> F:1431-1786/Region: heptad repeats F:1431-1786/Domain: I <DOM1> F:22/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted F:30-35/Disulfide bonds: #status predicted F:120,356,519,577,1041,1195,1279,1336,1343,1487,1533,1542,1643/Binding site: carbohydrate F:1179,1182,1785/Disulfide bonds: interchain #status predicted

Query Match 5.9%; Score 134; DB 1; Length 1786;
Best Local Similarity 20.9%; Pred No. 0.049;
Matches 84; Conservative 32; Mismatches 124; Indels 152; Gaps 24;
QY 21 GYLCKVTCETGDCRQBFDRSGNCVP-----CNOCGPGMELSKGFGYGED----- 69
DB 779 GSLSVCDPNGGQCQ-----CRPNVVGRTCNRCAPGT-----FGFGPNCKPC 821
QY 70 -----AQCVTCLRHFK-----EDNGFQKCKPC-----LDCAVNR 100
DB 822 DCHLQGSASFCDATGCHCFQGIYARQCRCPLGYPGFSPQSCQCQCHALDCDVTY- 880
QY 101 FOKANCATSDAI-----CGDCLPGFYRKTCLVGFDMCVCPGCDPPP-----YEPHCAS 151
DB 881 ---GECLSCDYTTGHCNERCLAGY-GDPIIGSD-HCRPCPCPDGSDSGRQFARSCYQ 935
QY 152 KYNLVKIASTASSPRDTALAAVICSALATVLLALLILCVYCKRQFMKKPSWLSRSDI 211
DB 936 DPVTIQLACVC---DPGYIGSRCD-----CASGFFGNPDSFGGSCQPC 976
QY 212 QYN-----GSELSC-----DRPOLHEYAH-----RAC----- 234
DB 977 QCHNHIDTDPACDKDGRCLUKLYHTEGDHCQICQCYGYGDALRQDCRCVCNWLGTV 1036
QY 235 -----CQCRSDSVQ-TCGPVRLPSMCCBEACSPNATI-----GGVHSAASLIQARN 281
DB 1037 KEHCNGSDCHCDKATGQCCLP-NVIGQNC--DRCAPNTWQLASGTGCGPCNCNA--AHS 1091
QY 282 AGPAGEMVPTFFGSLTQSIGFESDAWPLMQNPMGMDNISFC 323
DB 1092 FGPS-----CNEFTGCCQCMGP-FGGRCTCSEC 1117

RESULT 13
VWUU
von Willebrand factor precursor - human
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C:Accession: A34480; S02377; A37139; S23676; A25298; A25469; A25366; S23618; S23645; A94
R:Mancuso, D.J.; Tuley, E.A.; Westfield, L.A.; Worrall, N.K.; Shelton-Inloes, B.B.; Sor

J. Biol. Chem. 264, 19514-19527, 1989
A:Title: Structure of the gene for human von Willebrand factor.
A:Reference number: A34480; MUID:90062044
A:Accession: A34480
A:Molecule type: DNA
A:Residues: 1-2813 <MAN>
A:Cross-references: EMBL:M25864
R:Bonthron, D.; Orkin, S.H.
Eur. J. Biochem. 171, 51-57, 1988
A:Title: The human von Willebrand factor gene. Structure of the 5' region.
A:Reference number: S02377; MUID:88111704
A:Accession: S02377
A:Molecule type: DNA
A:Residues: 1-177 <BO2>
A:Cross-references: EMBL:X06828
R:Mancuso, D.J.; Tuley, E.A.; Westfield, L.A.; Lester-Mancuso, T.L.; Le Beau, M.M.; S
Biochemistry 30, 253-269, 1991
A:Title: Human von Willebrand factor gene and pseudogene: structural analysis and dif
A:Reference number: A37139; MUID:91105089
A:Accession: A37139
A:Molecule type: DNA
A:Residues: 990-1947 <MAD>
A:Cross-references: GB:M60675; NID:9340357; PIDN:AAA61295.1; PID:9553810
A:Note: The authors translated the codon CGC for residue 156 as Gln
R:Collins, C.J.; Underdahl, J.P.; Levene, R.B.; Ravera, C.P.; Morin, M.J.; Dombalagia
Proc. Natl. Acad. Sci. U.S.A. 84, 4393-4397, 1987
A:Title: Molecular cloning of the human gene for von Willebrand factor and identifica
A:Reference number: S23676; MUID:87260814
A:Accession: S23676
A:Molecule type: DNA
A:Residues: 2731-2813 <COL>
A:Cross-references: EMBL:M16945
R:Bonthron, D.; Orr, E.C.; Mitsock, L.M.; Ginsburg, D.; Handin, R.I.; Orkin, S.H.
Nucleic Acids Res. 14, 7125-7127, 1986
A:Title: Nucleotide sequence of pre-pro-von Willebrand factor cDNA.
A:Reference number: A25298; MUID:87016349
A:Accession: A25298
A:Molecule type: mRNA
A:Residues: 1-470, 'V', 472-2813 <BON>
A:Cross-references: EMBL:X04385
R:Verweij, C.L.; Diergaarde, P.J.; Hart, M.; Pannekoek, H.
EMBO J. 5, 1839-1847, 1986
A:Title: Full-length von Willebrand factor (vWF) cDNA encodes a highly repetitive pro
A:Reference number: A91044; MUID:87004550
A:Accession: A25469
A:Molecule type: mRNA
A:Residues: 1-470, 'V', 472-483, 'R', 485-1022, 'K', 1024-1025, 'E', 1027-1400 <VER>
A:Cross-references: EMBL:X04146
R:Verweij, C.L.; Diergaarde, P.J.; Hart, M.; Pannekoek, H.
EMBO J. 5, 3074, 1986
A:Reference number: A91056
A:Accession: A25366
A:Molecule type: mRNA
A:Residues: 1021-1030 <VE2>
A:Note: this is a revision to the sequence from reference A91044
R:Shelton-Inloes, B.B.; Broze Jr., G.J.; Miletich, J.P.; Sadler, J.E.
Biochem. Biophys. Res. Commun. 144, 657-665, 1987
A:Title: Evolution of human von Willebrand factor: cDNA sequence polymorphisms, repea
A:Reference number: S23618; MUID:87213253
A:Accession: S23618
A:Molecule type: mRNA
A:Residues: 1-120 <SH2>
A:Cross-references: EMBL:M17588; NID:g799330; PIDN:AAA65940.1; PID:g340316
A:Accession: S23645
A:Molecule type: protein
R:Sadler, J.E.; Shelton-Inloes, B.B.; Sorace, J.M.; Harlan, J.M.; Titani, K.; Davie,
Proc. Natl. Acad. Sci. U.S.A. 82, 6394-6398, 1985
A:Title: Cloning and characterization of two cDNAs coding for human von Willebrand fa
A:Reference number: A94060; MUID:86016708
A:Accession: A94060
A:Molecule type: mRNA

M62465; GB:M62466; GB:M62467; GB:M62468; GB:M62469; GB:M62470; NID:g511867; PIDN:AAA5061
R;Bornstein, P.; Alfli, D.; Devarayalu, S.; Framson, P.; Li, P.
J. Biol. Chem. 265, 16691-16698, 1990
A:Title: Characterization of the mouse thrombospondin gene and evaluation of the role of
A:Reference number: A37905; MUID:90375546
A:Accession: A37905
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-490 <BOR>
A:Cross-references: GB:J05605; GB:J05606; NID:g201991; PIDN:AAA40431.1; PID:g554390
R;Laherty, C.D.; O'Rourke, K.; Wolf, F.W.; Katz, R.; Seldin, M.F.; Dixit, V.M.
J. Biol. Chem. 267, 3274-3281, 1992
A:Title: Characterization of mouse thrombospondin 2 sequence and expression during cell
A:Reference number: A42587; MUID:92147683
A:Accession: B42587
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1152, P', 1154-1170 <LMS>
A:Cross-references: GB:M87276
A:Note: sequence extracted from NCBI backbone (NCBIP:81501)
R;Chen, H.; Aeschlimann, D.; Nowlen, J.; Mosher, D.F.
FEBS Lett. 387, 36-41, 1996
A:Title: Expression and initial characterization of recombinant mouse thrombospondin 1 a
A:Reference number: S68787; MUID:96234006
A:Accession: S68787
A:Molecule type: protein
A:Residues: 19-26, 'X', 28-37 <CHE>
C:Complex: homotrimer, disulfide linked
C:Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; v
C:Keywords: calcium binding; glycoprotein; homotrimer
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-1170/Product: thrombospondin 1 #status predicted <MAT>
F:317-375/Domain: von Willebrand factor type C repeat homology <VWC>
F:378-429/Domain: thrombospondin type 1 repeat homology <PHR1>
F:434-490/Domain: thrombospondin type 1 repeat homology <PHR2>
F:491-547/Domain: thrombospondin type 1 repeat homology <PHR3>
F:551-586/Domain: EGF homology <EGF>
F:248,360,708,1067/Binding site: carbohydrate (Asn) (covalent) #status predicted

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Best Local Similarity 21.0%; Pred. No. 0.04;
Matches 88; Conservative 39; Mismatches 141; Indels 151; Gaps 25;

Qy 26 KVTGTCRQOEFRDRSGNCPVNCQCPG-----MELSKCCGFGY----- 66
Db 350 KVSCEPIMPCSNATVPD--GEC--CPRCHPSDSDGWSHSEWTSCTATCGNGIQORGRS 405
Qy 67 -----GEDACQVTCRLH-----RFKEDWGFKQKPCLDCA-----VYVNRFOKAN-- 105
Db 406 CDSLNNRCGSSVQTRTCHIQCDKRFQDGGWSHSPSSCSVTGCGDGVITRILCNRP 465
Qy 106 -----CSATSDAICGDCPLPGFYRKTKL 127
Db 466 SPQNGKPCGEARETKACKDADKADPINCWGWSFDPWDCSVT-----CGG---GVQRRSRL 518
Qy 128 VGFQDMCEVCPGDPDPY-EPHCASKVNLVKIATSPRDTALAAVICSALATVLLALL 186
Db 519 -----CANNPTQFGKDCVGDVTENQVKNQKQDCPIDGCLSNP-CFAGAK----- 561
Qy 187 ILCVYIKRQFMKPKSWLSRQDIQYNGSELSCILDRPQLHE-----YAHRAQCOCRR-D 240
Db 562 --CTSY-----PDGSNKGACACPGYSGNGIQCKDQVDEKREVPDPCFNHNGEHRKNTD 612
Qy 241 SVQTC--GPVRLLP-----MCCCEACSP-NPATLG---CGVHSAASLQARNAGP 284
Db 613 PGYNCLPCPPPRFTGSPQFGRGVEHAMANKQVCKPRNPCTDGTDCNKNKAKNLYLGHYSDP 672
Qy 285 --AGEMVPTFFGSLTQSGEFS--DANPLMNPNGDNISF-----CDSYPELTGED 333
Db 673 MYRCECKFGYAGN--GLICGEDTDLGHP--NENLVCVANATYHCKKNCNPLNSGQED 728

RESULT 15
A60771
B-cell activation protein CD40 precursor - human
N:Alternate names: B-cell surface antigen Bp50
C:Species: Homo sapiens (man)
C:Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
C:Accession: S04460; A60771
R;Stamenkovic, I.; Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A:Title: A B-lymphocyte activation molecule related to the nerve growth factor recept
A:Reference number: S04460; MUID:89356608
A:Accession: S04460
A:Molecule type: mRNA
A:Residues: 1-277 <STA>
A:Cross-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851
R;Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-
A:Reference number: A60771; MUID:89093941
A:Accession: A60771
A:Molecule type: protein
A:Residues: 21-50 <BRA>
A:Experimental source: Burkitt lymphoma cell line Raji
C:Genetics:
A:Gene: GDB:CD40
A:Cross-references: GDB:215268; OMIM:109535
A:Map position: 20q12-20q13.2
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane prot
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
F:21-193/Domain: extracellular #status predicted <EXT>
F:194-215/Domain: transmembrane #status predicted <TMM>
F:216-277/Domain: intracellular #status predicted <CYT>
F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 5.8%; Score 132; DB 2; Length 277;
Best Local Similarity 24.6%; Pred. No. 0.0091;
Matches 52; Conservative 27; Mismatches 78; Indels 54; Gaps 11;

Qy 34 CRQOEFRDRSGNCPVNCQCPGMELSKECGYGEDACQVTCRLHRFKEDWG-----F 86
Db 26 CREKQYLINS-QC--CSLCQPCQKLVSDC--TEFTETCLPCGESEFLDTWNRETHCHQH 80
Qy 87 QKCKPCLDCAVVNRFOKANCSATSDAIC-----GDCPLPGFYRKTKL 127
Db 81 KYCDPNLGL-----RVQKGTSET-DTICTCEBGNHCTSEACESCVLHRSCSPGFGVKQIA 135
Qy 128 VGFQDMCEVCP-----GDPPPPY-----PHCASKVNLVKIAT-----ASSPRDTALAA 172
Db 136 TGVSDTICEPCVPGVFSNVSSAFKCHPWTSCETKDLVVQQAGTNKTDVCGPQDRLRAL 195
Qy 173 VICSALATVLLALLILCVYIKRQFMKPKS 203
Db 196 VWPIIFIGILFAILLVLVLFIRK---VAKKPT 223

Search completed: February 16, 2001, 21:06:44
Job time: 149 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 16, 2001, 21:09:26 ; Search time 19.12 seconds
(without alignments)
714.456 Million cell updates/sec

Title: US-09-380-276A-8
Perfect score: 2283
Sequence: 1 MALKVLEQEKFTFTLLVLL.....AIHPATQSLQVRQLGSL 423

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	157	6.9	454	1 TNRL_MOUSE	P25118 mus musculus
2	147	6.4	416	1 NGFR_HUMAN	P18519 gallus galli
3	146.5	6.4	1801	1 LMB2_RAT	P15800 rattus norv
4	145.5	6.4	435	1 TNRC_HUMAN	P36941 homo sapien
5	145	6.4	271	1 OX40_RAT	P15725 rattus norv
6	144	6.3	272	1 OX40_MOUSE	P47741 mus musculus
7	144	6.3	1104	1 NFX1_HUMAN	Q12986 homo sapien
8	141.5	6.2	461	1 TNRL_RAT	P22934 rattus norv
9	140	6.1	425	1 NGFR_RAT	P07174 rattus norv
10	137	6.0	1798	1 LMB2_HUMAN	P55268 homo sapien
11	134.5	5.9	415	1 TNRC_MOUSE	P50284 mus musculus
12	134	5.9	1786	1 LMB1_MOUSE	P02469 mus musculus
13	133.5	5.8	1799	1 LMB2_MOUSE	Q61292 mus musculus
14	133.5	5.8	2813	1 VWF_HUMAN	P04275 homo sapien
15	132.5	5.8	1170	1 TSPI_MOUSE	P35441 mus musculus
16	132	5.8	277	1 CD40_HUMAN	P25942 homo sapien
17	129	5.7	326	1 VT2_MVXVL	P29825 myxoma viru
18	128.5	5.6	1170	1 TSPI_HUMAN	P07996 homo sapien
19	127	5.6	4660	1 LRP2_RAT	P98158 rattus norv
20	126.5	5.5	471	1 TNRL_BOVIN	O19131 bos taurus
21	125.5	5.5	1173	1 TSPI_XENLA	P35448 xenopus lae
22	124.5	5.5	3712	1 LMA_DROME	Q00174 drosophila
23	122.5	5.4	1680	1 FUR2_DROME	P30432 drosophila
24	121	5.3	349	1 VC22_VARV	P34015 variola vir
25	121	5.3	1192	1 LMG2_MOUSE	Q61092 mus musculus
26	121	5.3	1964	1 NTC4_MOUSE	P31695 mus musculus
27	120.5	5.3	965	1 YNC3_YEAST	P53971 saccharomyc
28	120.5	5.3	2813	1 VWF_CANFA	Q28295 canis famil
29	120	5.3	256	1 41BB_MOUSE	P20334 mus musculus
30	119.5	5.2	1193	1 LMG2_HUMAN	Q13753 homo sapien
31	119	5.2	1786	1 LMB1_HUMAN	P07942 homo sapien
32	118.5	5.2	863	1 LDVR_CHICK	P98165 gallus gall
33	118	5.2	1592	1 SORL_CHICK	Q98930 g sortilin-

RESULT 1

ID	TNRL_MOUSE	STANDARD;	PRT;	454 AA.
AC	P25118;			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (TNF-RI) (P55).			
DE	(P55).			
GN	TNFRSF1A OR TNFR1 OR TNFR-1.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-91187885; PubMed-1849278;			
RA	Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,			
RA	Wong G.H., Chen E.Y., Goeddel D.V.;			
RT	"Cloning and expression of cDNAs for two distinct murine tumor			
RT	necrosis factor receptors demonstrate one receptor is species			
RT	specific.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-91246168; PubMed-1645445;			
RA	Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,			
RA	Copeland N.G., Jenkins N.A., Smith C.A.;			
RT	"Molecular cloning and expression of the type 1 and type 2 murine			
RT	receptors for tumor necrosis factor.";			
RL	Mol. Cell. Biol. 11:3020-3026(1991).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-91285014; PubMed-1647956;			
RA	Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissoneghis A.M.,			
RA	Gray P.W., Feldmann M., Foxwell B.M.J.;			
RT	"Cloning, expression and cross-linking analysis of the murine p55			
RT	tumor necrosis factor receptor.";			
RL	Eur. J. Immunol. 21:1649-1656(1991).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-SPLEEN;			
RX	MEDLINE-92039815; PubMed-1657766;			
RA	Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;			
RT	"Molecular cloning and expression of the mouse Tnf receptor type b.";			
RL	Immunogenetics 34:338-340(1991).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-94245292; PubMed-8188324;			
RA	Bebo B.F., Linthicum D.S.;			
RT	"Nucleotide sequence of the TNF type I receptor from a mouse			
RT	endothelioma cell line.";			
RL	Immunogenetics 39:450-451(1994).			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-93156721; PubMed-8381516;			
RA	Rothe J., Bluethmann H., Gentz R., Lesslauer W., Steinmetz M.;			

34	117.5	5.1	3075	1 LMAL_HUMAN	P25391 homo sapien
35	117	5.1	255	1 41BB_HUMAN	Q07011 homo sapien
36	116.5	5.1	1106	1 STC_DROME	P40798 drosophila
37	116	5.1	417	1 WSCI_HUMAN	Q93038 h wsl-1 pro
38	116	5.1	1790	1 LMB1_DROME	P11046 drosophila
39	114.5	5.0	1557	1 LMB1_CAEL	Q18823 caenorhabdi
40	114	5.0	327	1 FASA_MOUSE	P25446 mus musculus
41	114	5.0	455	1 TNRL_HUMAN	P19438 homo sapien
42	113.5	5.0	427	1 NGFR_HUMAN	P08138 homo sapien
43	113	4.9	4753	1 LRP_CAEL	Q04833 caenorhabdi
44	112.5	4.9	3635	1 LMA5_MOUSE	Q61001 mus musculus
45	112	4.9	461	1 TNRL_PIG	P50555 sus scrofa

ALIGNMENTS

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```

CC DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).
CC GN TNFRSF4 OR TNXPIL OR OX40.
CC OS Rattus norvegicus (Rat).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CC -----
DR EMBL; L04270; AAA36757.1; -.
DR HSP; P25942; ICDP.
DR MIN; 600979; -.
DR INTERPRO; IPR001368; -.
DR PFAM; PF00020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 30
FT CHAIN 31 435
FT DOMAIN 31 227
FT TRANSMEM 228 248
FT DOMAIN 249 435
FT DOMAIN 42 211
FT REPEAT 42 81
FT REPEAT 82 124
FT REPEAT 125 168
FT REPEAT 169 211
FT DISULFID 43 58
FT DISULFID 59 72
FT DISULFID 62 80
FT DISULFID 83 98
FT DISULFID 101 116
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FT DISULFID 126 132
FT DISULFID 139 148
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FT DISULFID 170 185
FT CARBOHYD 40 40
FT CARBOHYD 177 177
SQ SEQUENCE 435 AA; 46709 MW; 624626E6022F656F CRC64;

Query Match 6.4%; Score 145.5; DB 1; Length 435;
Best Local Similarity 21.4%; Pred. No. 0.00042;
Matches 73; Conservative 41; Mismatches 108; Indels 119; Gaps 19;

QY 16 LVLVGLYLSCK-----VTCETGCRQOE---FDRSGNVCVPCNOCGPGMELSKCEGFG 65
DB 18 VLGLFGLLAASQAPVPPYASENQCRCQKEYYEPQHRIC--CSRCPPTGVYSAKC--S 73
QY 66 YGEDAQCVTCRLHREKEDWGF---QKCKPC-----LDCAVNVNRFQKANCATSDAIC- 114
DB 74 RIRDIVCATCAENSNEHWNLYTICQLCRPCDPVMGLEEIAPICTSKRTQCRQCPMFC 133
QY 115 -----GDCPLPGFYRKTK-LVGFQDMCEVPC-----GDPPPPPYEPH--CAS 151
DB 134 AWALECTHCELLSDCPGTEAEALKEVGKGNHVCPCKAGHFQNTSSPSARCPHTRCEN 193
QY 152 KYNLVKIA-----STASSPRD-----TALAATVCSALATVLLALLILCVIY---- 192
DB 194 Q-GLVEAAPGTAQSDTCKNPLEPLPEMSGTMLMLAVLLPLAFFLLATVFCISWKSH 252
QY 193 --CKR--QFMKKP-----SWSLRSDIQNGSELSCLDRLPOLHEVAHRAHCCQCR 238
DB 253 SLCKRLGSLKKRRPOGEGNPNVAGSW-----EPKAPHYF----- 287
QY 239 RDSVQTGCVRLPSPMCCEAEASPNPATLGGCVHSAASLQA 279
DB 288 PDLVQPLLP-----SGDVSPVSTGLPAAPVLEA 316

RESULT 5
OX40_RAT
ID OX40_RAT STANDARD; PRT; 271 AA.
AC P15725;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)

```

```

DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).
GN TNFRSF4 OR TNXPIL OR OX40.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN SEQUENCE FROM N.A.
RP TISSUE-T-CELL;
RX MEDLINE=90214614; PubMed=2157591;
RA Mallett S., Fossum S., Barclay A.N.;
RT "Characterization of the MRC OX40 antigen of activated CD4 positive T
RL Lymphocytes -- a molecule related to nerve growth factor receptor.";
EMBO J. 9:1063-1068(1990).
CC -!- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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RESULT 6
OX40_MOUSE

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ID OX40_MOUSE STANDARD; PRT; 272 AA.
AC P47741;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).
GN TNFRSF4 OR TXGP1 OR OX40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=94044750; PubMed=8228223;
RA Calderhead D.M., Buhmann J.E., van den Eertwegh A.J.,
RT Claassen E., Noelle R.J., Fell H.;
RT "Cloning of mouse OX40: a T cell activation marker that may mediate
RT T-B cell interactions.";
RL J. Immunol. 151:5261-5271(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95255413; PubMed=7737295;
RA Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Barclay A.N.;
RT "Gene structure and chromosomal localization of the mouse homologue
RT of rat OX40 protein.";
RL Eur. J. Immunol. 25:926-930(1995).
CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC -----
CC EMBL; Z21674; CAA79772.1; -
CC EMBL; X85214; CAA59476.1; -
CC HSSP; P25942; ICDF.
CC MGD; MGI:104512; TXGP1.
CC INTERPRO; IPR001368; -
CC PFAM; PF00020; TNFR_C6; 3.
CC PROSITE; PS00652; TNFR_NGFR_1; 3.
CC PROSITE; PS50050; TNFR_NGFR_2; 2.
CC Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
CC Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 272 OX40L RECEPTOR.
FT DOMAIN 20 211 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 212 236 POTENTIAL.
FT DOMAIN 237 272 CYTOPLASMIC (POTENTIAL).
FT REPEAT 26 165 4 X TNFR-CYS.
FT REPEAT 26 61 TNFR-CYS 1.
FT REPEAT 62 103 TNFR-CYS 2.
FT REPEAT 104 124 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 125 165 TNFR-CYS 4.
FT CARBOHYD 144 144 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 15 15 A -> G (IN REF. 2).
FT SEQUENCE 272 AA; 30153 MW; 06E7BB4156F0D08E CRC64;
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Query Match 6.3%; Score 144; DB 1; Length 272;
Best Local Similarity 29.5%; Pred. No. 0.00033;
Matches 54; Conservative 21; Mismatches 76; Indels 32; Gaps 13;

```
QY 15 TLVLVLLGYSCKVTCTGDCRQOEFRDRSGN-CVPCNQCQPGMELSKGCGFGYGEDAQCV 73
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 9 TALLLLA-LTLGVTARRLNCVKHTY--PSGKHC--CRECOPGHGMYSRC--DHTRTDLCH 61
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 74 TCRLHRFKEDWGFQKCKPCLDCAVVRFO-KANCSATSDAICGDCPLPGFYRKYTKLVGFOD 132
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Db 62 PCETGFYNEAVNYDTCKQCTQCNRHSGSELKQNCCTPTQDTVC-RCRPGTQPR-----QD 114
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 133 -----MECVPCGDPDPPEP-----HCASKVNLVKLTASTASSPRDTALAIVC---SALA 179
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 115 SGYKLGVDVCPC--PPGHFSPGNACKPWTNCTLSGKOTRHPASDLSLDAV-CEDRSLLA 171
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 180 TVL 182
| | |
DB 172 TLL 174
| | |
RESULT 7
ID NFXL_HUMAN STANDARD; PRT; 1104 AA.
AC O12986;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE TRANSCRIPTIONAL REPRESSOR NF-X1.
GN NFXL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95053707; PubMed=7964459;
RA Song Z., Krishna S., Thanos D., Strominger J.L., Ono S.J.;
RT "A novel cysteine-rich sequence-specific DNA-binding protein
RT interacts with the conserved X-box motif of the human major
RT histocompatibility complex class II genes via a repeated Cys-His
RT domain and functions as a transcriptional repressor.";
RL J. Exp. Med. 180:1763-1774(1994).
CC -1- FUNCTION: REPRESSOR OF HLA-DRA TRANSCRIPTION. BINDS TO THE X-BOX
CC MOTIF OF CLASS II MHC GENES. MAY PLAY AN IMPORTANT ROLE IN
CC REGULATING THE DURATION OF AN INFLAMMATORY RESPONSE BY LIMITING
CC THE PERIOD IN WHICH CLASS II MHC MOLECULES ARE INDUCED BY
CC INTERFERON-GAMMA.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- INDUCTION: BY INTERFERON-GAMMA.
CC -1- SIMILARITY: TO D.MELANOGASTER SHUTTLE CRAFT PROTEIN (STC) AND
CC YEAST YNL023C.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U15306; AAA69517.1; -
CC HSSP; P02876; 2WGC.
CC INTERPRO; IPR000967; -
CC INTERPRO; IPR001374; -
CC PFAM; PF01424; R3H; 1.
CC PFAM; PF01422; zf-NF-X1; 8.
CC Transcription regulation; Repressor; DNA-binding; Nuclear protein;
CC Repeat.
FT DOMAIN 424 876 7 X APPROXIMATE REPEATS, CYS-RICH.
FT REPEAT 424 463 1.
FT REPEAT 480 517 2.
FT REPEAT 541 580 3.
FT REPEAT 606 647 4.
FT REPEAT 695 734 5.
FT REPEAT 806 842 6.
FT REPEAT 836 876 7.
FT SEQUENCE 1104 AA; 123149 MW; 36FEC4292F78130C CRC64;
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Query Match 6.3%; Score 144; DB 1; Length 1104;
Best Local Similarity 18.8%; Pred. No. 0.0016;
Matches 110; Conservative 59; Mismatches 181; Indels 236; Gaps 27;

QY 24 SKVCTGTGCRQOEFRDRSGNVCPCNQCPCGPMELSKCQ-----FGYGEDAQ----- 72
DB 440 SCNLLCHPG-----PCPCFAFTKCECGRTRHTVPCGAVSHCSNPC 484
QY 73 ---VTCRLHREFKEDWQKCKPCLDCAVNRKANCATS-DAICGDCPLPGFYRKTKLV 128
DB 485 ENILNCQHQCAELCHGGCQPCQ---IILN-QVCYGGTSRDVLCTGDV-----GKSD 534
QY 129 GFQDMEC-----VPCGD-----PPHPC-ASKVNLVKIATASS 164
DB 535 GFGDFCLTKCGKDLKCGNHTCSOVCHPCQPCQPRLPQLVRCPCGQTLPSQLLELSS 594
QY 165 PROTALAAV-----IC-SALATVLLALLILC-----VIVCKRQFMKK- 201
DB 595 SRKTCMDPVSCGKVCCKPLPCGSLDPIHTCEKLCHEGDCGVPVSRVTSICRCSFRTEL 654
QY 202 PWSLRSQDI-----QYNGSELSCDRPQ-----LH---EYA 230
DB 655 PCTSLKSEDATFMDCKRCKKRLCGRHCKNEICCVDRKHCPLNCGRKLRCGLHRCBEP 714
QY 231 HRACCO-CRDSVQT-----CGVRLPSMCC-----EE 258
DB 715 HRGNCQTCWQASEDELTCGASVIYPPVCGTRRPPCTQTCARVHCDHPVYHSGHSE 774
QY 259 ACS-----PNTATLCCGVHSAASL----- 277
DB 775 KCPCTELTKQWCKGHEFRSNIPCHLVDSGLPLCSATLPCGHHKQRLCHKGECLVDE 834
QY 278 -----QAR-----NAGPAGEWVPTFFGSLFQSI 300
DB 835 PCKQCTTPRADCGHPCWAPCHTSSPCVPTACKAKVELQCEGRRKEMVICSEASSTYQR 894
QY 301 CGEFSDAWPLMOPMGDNISFCDSYFELTGEDIHSLNPELESSTLDSNSSQDLVGAV 360
DB 895 IAAISMASKITDMOLGGS-----VEISKLTKEVHQARLECECSALEKRKR--LAEAF 948
QY 361 PVOSHSENTAATDLSRYNNTLVESATQDALTMRSOLDQESGAI 406
DB 949 HISEDSPFNIRSSGSFKFSDSLKEDA--RKDLKFVSDVERKEMETLV 992
RESULT 8
TNRL_RAT
ID TNRL_RAT STANDARD; PRT; 461 AA.
AC P22934:
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-RI) (TNF-RI)
DE (P55).
GN TNFRSF1A OR TNFR1 OR TNFR-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91090841; PubMed-1702293;
RA Himmeler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,
RA Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;
RT "Molecular cloning and expression of human and rat tumor necrosis
RT factor receptor chain (p60) and its soluble derivative, tumor
RL necrosis factor-binding protein.";
RL DNA Cell Biol. 9:705-715(1990).
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY

CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC NF-KAPPA B SIGNALING (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC
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CC
CC EMBL; MG3122; AAA42256.1; -
DR PIR; B36555; B36555.
DR HSP; P19438; ITNR.
DR INTERPRO; IPR000488; -
DR INTERPRO; IPR001368; -
DR PFAM; PF00020; TNFR_c6; 4.
DR PFAM; PF00531; death; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
FT SIGNAL 1 21
FT CHAIN 22 461
FT DOMAIN 22 211
FT TRANSMEM 212 234
FT DOMAIN 235 461
FT DOMAIN 43 196
FT REPEAT 43 82
FT REPEAT 83 125
FT REPEAT 126 166
FT REPEAT 167 196
FT REPEAT 344 354
FT DOMAIN 363 448
FT DISULFID 44 58
FT DISULFID 59 72
FT DISULFID 62 81
FT DISULFID 84 99
FT DISULFID 102 117
FT DISULFID 105 125
FT DISULFID 127 143
FT DISULFID 146 158
FT DISULFID 149 166
FT DISULFID 168 179
FT DISULFID 182 191
FT DISULFID 185 195
FT CARBOHYD 54 54
FT CARBOHYD 151 151
FT CARBOHYD 201 201
SQ SEQUENCE 461 AA; 50969 MW; EB23C05450FBD202 CRC64;
Query Match 6.2%; Score 141.5; DB 1; Length 461;
Best Local Similarity 21.6%; Pred. No. 0.00092;
Matches 72; Conservative 37; Mismatches 113; Indels 111; Gaps 20;
QY 34 CROQEFDRSGNVCPCNQCPCGPMELSKCQFGYGEDAQCVTCRLHREFKEDWQKCKPCL 93
DB 44 CPQKRYAHKPNKNSICCTKCHKGTYLVSDCP-SPQGETVCEVCDKGTFTASQ--NHVROCL 100
QY 94 DCAYVNR--FQK---ANGSATSDAICGDCPLPGFYRKTKLVGFGDMCEVPC----- 138
DB 101 SKCTCRKEMFQVEISPCKADMDTVCGCKKNQFQRYLSETHFCQVDCSPCFNGTVPICKE 160
QY 139 -----GDPPIPPYEPHCASKVNLVKI-----ASTASSPRDTAAAVICSALA 179
DB 161 KONTVCNCHAGFFLSGNECTPCS-HCKKNQCBMKLCLPPVANVTNPQDSGTAVLLPLVIF 219

DR	PROSITE; PS00652; TNFR_NGFR_1; 3.	FT	CHAIN	1	29	FT	CHAIN	30	425	FT	LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR.	FT	DOMAIN	30	251	FT	EXTRACELLULAR (POTENTIAL).	FT	TRANSMEM	252	273	FT	POTENTIAL.	FT	DOMAIN	274	425	FT	CYTOPLASMIC (POTENTIAL).	FT	DOMAIN	32	190	FT	4 X TNFR-CYS.	FT	REPEAT	32	66	FT	TNFR-CYS 1.	FT	REPEAT	67	108	FT	TNFR-CYS 2.	FT	REPEAT	109	148	FT	TNFR-CYS 3.	FT	REPEAT	149	190	FT	TNFR-CYS 4.	FT	DOMAIN	198	249	FT	SER/THR-RICH.	FT	DOMAIN	354	419	FT	DEATH DOMAIN.	FT	DISULFID	33	44	FT	BY SIMILARITY.	FT	DISULFID	45	58	FT	BY SIMILARITY.	FT	DISULFID	48	65	FT	BY SIMILARITY.	FT	DISULFID	68	84	FT	BY SIMILARITY.	FT	DISULFID	87	100	FT	BY SIMILARITY.	FT	DISULFID	90	108	FT	BY SIMILARITY.	FT	DISULFID	110	123	FT	BY SIMILARITY.	FT	DISULFID	126	139	FT	BY SIMILARITY.	FT	DISULFID	129	147	FT	BY SIMILARITY.	FT	DISULFID	150	165	FT	BY SIMILARITY.	FT	DISULFID	168	181	FT	BY SIMILARITY.	FT	DISULFID	171	189	FT	BY SIMILARITY.	FT	CARBOHYD	61	61	FT	N-LINKED (GLCNAC. .) (POTENTIAL).	FT	CARBOHYD	71	71	FT	N-LINKED (GLCNAC. .) (POTENTIAL).	FT	SEQUENCE	425 AA; 45432 MW; B2E152D94D3827F8 CRC64;	QY
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.	FT	CHAIN	1	29	FT	CHAIN	30	425	FT	LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR.	FT	DOMAIN	30	251	FT	EXTRACELLULAR (POTENTIAL).	FT	TRANSMEM	252	273	FT	POTENTIAL.	FT	DOMAIN	274	425	FT	CYTOPLASMIC (POTENTIAL).	FT	DOMAIN	32	190	FT	4 X TNFR-CYS.	FT	REPEAT	32	66	FT	TNFR-CYS 1.	FT	REPEAT	67	108	FT	TNFR-CYS 2.	FT	REPEAT	109	148	FT	TNFR-CYS 3.	FT	REPEAT	149	190	FT	TNFR-CYS 4.	FT	DOMAIN	198	249	FT	SER/THR-RICH.	FT	DOMAIN	354	419	FT	DEATH DOMAIN.	FT	DISULFID	33	44	FT	BY SIMILARITY.	FT	DISULFID	45	58	FT	BY SIMILARITY.	FT	DISULFID	48	65	FT	BY SIMILARITY.	FT	DISULFID	68	84	FT	BY SIMILARITY.	FT	DISULFID	87	100	FT	BY SIMILARITY.	FT	DISULFID	90	108	FT	BY SIMILARITY.	FT	DISULFID	110	123	FT	BY SIMILARITY.	FT	DISULFID	126	139	FT	BY SIMILARITY.	FT	DISULFID	129	147	FT	BY SIMILARITY.	FT	DISULFID	150	165	FT	BY SIMILARITY.	FT	DISULFID	168	181	FT	BY SIMILARITY.	FT	DISULFID	171	189	FT	BY SIMILARITY.	FT	CARBOHYD	61	61	FT	N-LINKED (GLCNAC. .) (POTENTIAL).	FT	CARBOHYD	71	71	FT	N-LINKED (GLCNAC. .) (POTENTIAL).	FT	SEQUENCE	425 AA; 45432 MW; B2E152D94D3827F8 CRC64;	QY
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.	FT	CHAIN	1	29	FT	CHAIN	30	425	FT	LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR.	FT	DOMAIN	30	251	FT	EXTRACELLULAR (POTENTIAL).	FT	TRANSMEM	252	273	FT	POTENTIAL.	FT	DOMAIN	274	425	FT	CYTOPLASMIC (POTENTIAL).	FT	DOMAIN	32	190	FT	4 X TNFR-CYS.	FT	REPEAT	32	66	FT	TNFR-CYS 1.	FT	REPEAT	67	108	FT	TNFR-CYS 2.	FT	REPEAT	109	148	FT	TNFR-CYS 3.	FT	REPEAT	149	190	FT	TNFR-CYS 4.	FT	DOMAIN	198	249	FT	SER/THR-RICH.	FT	DOMAIN	354	419	FT	DEATH DOMAIN.	FT	DISULFID	33	44	FT	BY SIMILARITY.	FT	DISULFID	45	58	FT	BY SIMILARITY.	FT	DISULFID	48	65	FT	BY SIMILARITY.	FT	DISULFID	68	84	FT	BY SIMILARITY.	FT	DISULFID	87	100	FT	BY SIMILARITY.	FT	DISULFID	90	108	FT	BY SIMILARITY.	FT	DISULFID	110	123	FT	BY SIMILARITY.	FT	DISULFID	126	139	FT	BY SIMILARITY.	FT	DISULFID	129	147	FT	BY SIMILARITY.	FT	DISULFID	150	165	FT	BY SIMILARITY.	FT	DISULFID	168	181	FT	BY SIMILARITY.	FT	DISULFID	171	189	FT	BY SIMILARITY.	FT	CARBOHYD	61	61	FT	N-LINKED (GLCNAC. .) (POTENTIAL).	FT	CARBOHYD	71	71	FT	N-LINKED (GLCNAC. .) (POTENTIAL).	FT	SEQUENCE	425 AA; 45432 MW; B2E152D94D3827F8 CRC64;	QY
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.	FT	CHAIN	1	29	FT	CHAIN	30	425	FT	LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR.	FT	DOMAIN	30	251	FT	EXTRACELLULAR (POTENTIAL).	FT	TRANSMEM	252	273	FT	POTENTIAL.	FT	DOMAIN	274	425	FT																																																																																																																																			


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RESULT 12
LMBL_MOUSE
AC P02469; STANDARD; PRT: 1786 AA.
DT 01-JUL-1986 (Rel. 01, Last Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN).
GN LAMB1-1 OR LAMB-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE-87147212; PubMed-3493487;
RA Sasaki M., Kato S., Kohno K., Martin G.R., Yamada Y.;
RT "Sequence of the cDNA encoding the laminin B1 chain reveals a
multidomain protein containing cysteine-rich repeats.";
Proc. Natl. Acad. Sci. U.S.A. 84:935-939(1987).
[2]
RP SEQUENCE OF 1292-1786 FROM N.A.
RX MEDLINE-85051302; PubMed-6209134;
RA Barlow D.P., Green N.M., Kurkinen M., Hogan B.L.M.;
RT "Sequencing of laminin B chain cDNAs reveals C-terminal regions of
coiled-coil alpha-helix.";
EMBO J. 3:2355-2362(1984).
[3]
RP SEQUENCE OF 165-172; 539-547 AND 712-719.
RX STRAIN-BALB/C; TISSUE-ENDOTHELIAL CELLS;
RC MEDLINE-97363207; PubMed-9219532;
RA Frieser M., Noeckel H., Pausch F., Roeder C., Hahn A., Deutzmann R.,
RA Sorokin L.M.;
RT "Cloning of the mouse laminin alpha 4 cDNA. Expression in a subset of
endothelium.";
Eur. J. Biochem. 246:727-735(1997).
CC -!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR. LAMININ
IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
CC -!- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
CC THE BETA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMININ), LAMININ-
2 (MEROSIN), AND LAMININ-6 (K-LAMININ).
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
COMPONENT).
CC -!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC -!- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
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or send an email to license@isb-sib.ch).
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DR EMBL; M15525; AAA39407.1; ALT_INIT.
DR EMBL; X05212; CAA28839.1; -.
DR PIR; A26413; MMSB1.
DR HSP; P03069; IZIM.
DR MGD; MGI:96743; LAMB1-1.
DR INTERPRO; IPR000561; -.
DR INTERPRO; IPR001886; -.
DR INTERPRO; IPR002049; -.
DR PFW; PF00053; laminin_EGF; 13.
DR PFW; PF00055; laminin_Nterm; 1.
DR PRINTS; PR00011; EGF-LAMININ.
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PROSITE; PS00022; EGF_1; 9.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 1786 LAMININ BETA-1 CHAIN.
FT DOMAIN 22 270 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 271 540 4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN V).
FT DOMAIN 271 334 LAMININ EGF-LIKE 1.
FT DOMAIN 335 397 LAMININ EGF-LIKE 2.
FT DOMAIN 398 457 LAMININ EGF-LIKE 3.
FT DOMAIN 458 509 LAMININ EGF-LIKE 4.
FT DOMAIN 510 540 LAMININ EGF-LIKE 5 (INCOMPLETE).
FT DOMAIN 541 772 LAMININ DOMAIN IV.
FT DOMAIN 773 1178 8 X LAMININ EGF-LIKE REPEATS (DOMAIN III).
FT DOMAIN 773 820 LAMININ EGF-LIKE 6.
FT DOMAIN 821 866 LAMININ EGF-LIKE 7.
FT DOMAIN 867 916 LAMININ EGF-LIKE 8.
FT DOMAIN 917 975 LAMININ EGF-LIKE 9.
FT DOMAIN 976 1027 LAMININ EGF-LIKE 10.
FT DOMAIN 1028 1083 LAMININ EGF-LIKE 11.
FT DOMAIN 1084 1131 LAMININ EGF-LIKE 12.
FT DOMAIN 1132 1178 LAMININ EGF-LIKE 13.
FT DOMAIN 1179 1397 DOMAIN II.
FT DOMAIN 1398 1430 DOMAIN ALPHA.
FT DOMAIN 1431 1786 DOMAIN I.
FT DOMAIN 1216 1315 COILED COIL (POTENTIAL).
FT DOMAIN 1368 1388 COILED COIL (POTENTIAL).
FT DOMAIN 1448 1778 COILED COIL (POTENTIAL).
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FT DISULFID 976 990 BY SIMILARITY.
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FT DISULFID 1117 1129 BY SIMILARITY.
FT DISULFID 1132 1144 BY SIMILARITY.

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FT DISULFID 1134 1151 BY SIMILARITY.
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FT DISULFID 1165 1176 BY SIMILARITY.
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FT DISULFID 1182 1182 INTERCHAIN (PROBABLE).
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FT DISULFID 1785 1785 INTERCHAIN (PROBABLE).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 519 519 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 677 677 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1041 1041 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1195 1195 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1279 1279 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1336 1336 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1343 1343 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1487 1487 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1533 1533 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1542 1542 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1643 1643 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 1531 1534 SGNA -> MEMP (IN REF. 2).
FT CONFLICT 1749 1749 D -> N (IN REF. 2).
SQ SEQUENCE 1786 AA; 196904 MW; 846671B7BF41A474 CRC64;

Query Watch 5.9%; Score 134; DB 1; Length 1786;
Best Local Similarity 20.9%; Pred. No. 0.016;
Matches 84; Conservative 32; Mismatches 124; Indels 162; Gaps 24;

QY 21 GYLSCKVTCTGCRQGFDRSGNCP-----CNCQGGMELSKCEGFGYGED----- 69
DB 779 GSLSSVCDPNNGQCQ-----CRPNVVGRTCNRCAPGT-----FGFGNGCKPC 821
QY 70 -----ACQVTCRLHREK-----EDWGFQCKPC-----LDCAVVNR 100
DB 822 DCHLQGSASAFCDRTGQCHFGIYARQCDRLPGYWGFPSCQCGNCHALDCDVT- 880
QY 101 FOKANGSATSDAI-----CGDCLPGFYKTKLVGFQDMCVPCGDDPPPP-----YEPHCAS 151
DB 881 ---GECLSCQDYTTGHCNRCERLAGYV-GDPIIGSGD-HCRPCPCPDGPDGQGFARSCYQ 935
QY 152 KVNLVKIATSSPRDTALAANVCSALATVLLALLILCVYCKRQFWEKPKPSLSRSQDI 211
DB 936 DPTVLQLACVC-----DPGYTGRCDP-----CASGFFGNPSDFGGSCQPC 976
QY 212 QYN-----GSELSCL-----DRPQLHEYAH-----RAC----- 234
DB 977 QCHNIDTTDPEACDRDTGRLCLKLVHTGDCQCLQCYGYGDALRQDCRKCVCNVLGTV 1036
QY 235 -----CQCRDVSQV-TGCPVRLPLSPMCCEACSPNPATL-----GCGVHSAASLQARN 281
DB 1037 KEHNGSDCHDKATGQCSCLP-NVIGQNC--DRCAPNTWOLASGTGCGPCNCNA--AHS 1091
QY 282 AGPAGEWPTFFGSLTQSGEFSDAWPLMNPMPGDNISFC 323
DB 1092 FGPS-----CNEFTGQCQCPMG-FGGRTCSEC 1117

RESULT 13
LMB2_MOUSE
ID LMB2_MOUSE STANDARD; PRT: 1799 AA.
AC Q61292; Q62182;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE LAMININ BETA-2 CHAIN PRECURSOR.
GN LAMB2 OR S-LAM OR LAMS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/J;
RX MEDLINE=96278760; PubMed=8662701;
..

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RA Durkin M.E., Gautam M., Loechel S., Sanes J.R., Merlie J.P.,
RA Albrechtsen R., Wewer U.M.;
RT "Structural organization of the human and mouse laminin beta2 chain
RT genes, and alternative splicing at the 5' end of the human
RT transcript.;"
RL J. Biol. Chem. 271:13407-13416(1996).
RN [2]
RN SEQUENCE OF 348-428 FROM N.A.
RX TISSUE=LUNG;
RX MEDLINE=94319092; PubMed=8043959;
RA Aberdam D., Galliano M.F., Mattei M.-G., Ortonne J.P., Meneguzzi G.;
RT "S-laminin gene (lams) maps to F1 band of mouse chromosome 9.;"
RL Mamm. Genome 5:393-394(1994).
RN [3]
RN FUNCTION.
RC STRAIN=129/J;
RC MEDLINE=95191550; PubMed=7885444;
RA Noakes P.G., Gautam M., Mudd J., Sanes J.R., Merlie J.P.;
RT "Aberrant differentiation of neuromuscular junctions in mice lacking
RT s-laminin/laminin beta 2.;"
RL Nature 374:258-262(1995).
CC -!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ
CC IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
CC CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
CC WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
CC -!- FUNCTION: LAMININ-3 (S-LAMININ) REGULATES THE FORMATION OF MOTOR
CC NERVE TERMINALS.
CC -!- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
CC DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
CC TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
CC COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
CC THE BETA-2 CHAIN IS A SUBUNIT OF LAMININ-3 (S-LAMININ), LAMININ-4
CC (S-MEROSIN), AND LAMININ-7 (KS-LAMININ).
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT
CC MEMBRANES (MAJOR COMPONENT).
CC -!- TISSUE SPECIFICITY: NEUROMUSCULAR SYNAPSE AND KIDNEY GLOMERULUS.
CC -!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC -!- DOMAIN: DOMAINS VI AND IV ARE GLOBULAR.
CC -!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
CC -!- SIMILARITY: CONTAINS 12.5 LAMININ EGF-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U43541; AAC53535.1;
CC EMBL; U42624; AAC53535.1; JOINED.
CC EMBL; X75928; CAAS3532.1;
CC HSP; P02468; IKLO.
CC MGI; 99916; LAMB2.
CC INTERPRO: IPR000561;
CC INTERPRO: IPR001886;
CC INTERPRO: IPR002049;
CC PFAM; PF00053; laminin_EGF; 13.
CC PFAM; PF00055; laminin_Nterm; 1.
CC PRINTS; PR00011; EGFLAMININ.
CC PROSITE; PS00022; EGF_1; 10.
CC PROSITE; PS01186; EGF_2; 2.
CC PROSITE; PS01248; LAMININ_TYPE_EGF; 12.
CC Glycoprotein; Basement membrane; Extracellular matrix; Coiled coll;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT SIGNAL 1 35 POTENTIAL.
FT CHAIN 36 1799 LAMININ BETA-2 CHAIN.
FT DOMAIN 36 283 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 284 555 4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
FT V).
FT DOMAIN 286 349 LAMININ EGF-LIKE 1.

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FT	CARBOHYD	1349	1349	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1500	1500	N-LINKED (GLCNAC. . .) (POTENTIAL).
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Query Match 5.8%; Score 133.5; DB 1; Length 1799;				
Best Local Similarity 20.1%; Pred. No. 0.017;				
Matches 92; Conservative 40; Mismatches 121; Indels 205; Gaps 27;				
QY	17	LVLLGYLSCKVTCTGDCRQOQFRDRSNCVPCNQCGPMGELSKEG	-----GFGQ---	65
DB	776	LIYNGALPCQ--CDPQSLSECSPHGGQC	-----RCKPGV-VGRCDVCAATGYVGGPAG	828
QY	66	-----XGEDAQCVTCRLHFR	-----KEDMGFQKCKPCLDCAVVNRF	101
DB	829	CQACQCSPDGALSALCEGTSGQC-PCRPGAFGLRCDHCQGMGFPCNRCPCV	-----	879
QY	102	KQANCATSATSDAI	-----CGDCLPGFYRKTKL-VGFQDMECVPCGDPP	142
DB	880	-----CNGRADECDTHTGACLCGRDYTGGEHCERCIAGFDGPRLPYGGQ	-----CRPCPCPE	932
QY	143	PPVEPHCASKVNLVKIATASTASPRDTALAAVICSALATVLLALLLCVIVCKRQEM	-----	198
DB	933	GPGSORHFAT	-----SCHRDGYSQIIVC	965
QY	199	-----EKKP	-----SWSLRSQDIO	224
DB	966	CEACAPGPFPGDPSPGGRQCCEGSGNIDPMDPDACDPHTGQCLRLHNTGEPHCGYCKP	-----	1025
QY	225	QLH-EYAHRACCQCRSRDSVQTCGPVRLPSMC	-----CE	259
DB	1026	GFGQAARQSCIRC	-----TCNLLGTDRRCRSTDLCHCDPSTGQCPLPHVQGLNCDH	1079
QY	260	CSPN-PATLGGVHSAASLQARNAGP	-----AGEMYPTFGSITQSGICEFS	305
DB	1080	CAPFNWETSGRCQPCACHPSRARGPTCNFTGQCCHCAG	-----FGRTCECOELY	1133
QY	306	DAWPLMQ	-----NPMGGD	331
DB	1134	WGDPGLQCRACDCDPRGIDKQCHRSCTGCHSCRPVSG	1171	
RESULT 14				
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ID	VWF_HUMAN	STANDARD;	PRT; 2813 AA.	
AC	P04275;			
DT	20-MAR-1987	(Rel. 04, Created)		
DT	01-JUL-1993	(Rel. 26, Last sequence update)		
DT	01-OCT-2000	(Rel. 40, Last annotation update)		
DE	VON WILLEBRAND FACTOR PRECURSOR (VWF).			
GN	F8VWF OR VWF.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
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RP	SEQUENCE FROM N.A.			
RA	MEDLINE=90062044; PubMed=2584182;			
RX	Mancuso D.J., Tuley E.A., Westfield L.A., Worrall N.K.,			
RA	Shelton-Inloes B.B., Sorace J.M., Alevy Y.G., Sadler J.E.;			
RT	"Structure of the gene for human von Willebrand factor.;"			
RL	J. Biol. Chem. 264:19514-19527(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=87016349; PubMed=3489923;			
RA	Bonthron D., Orr E.C., Mitsock L.M., Ginsburg D., Handin R.I.,			
RT	Orkin S.H.;			
RL	"Nucleotide sequence of pre-pro-von Willebrand factor cDNA.;"			
RN	[3]			
RP	SEQUENCE OF 1-120 FROM N.A., AND SEQUENCE OF 23-56.			
RC	TISSUE-UMBILICAL VEIN ENDOTHELIAL CELLS;			
RX	MEDLINE=87213253; PubMed=3495266;			
RA	Shelton-Inloes B.B., Broze G.J., Milewich J.P., Sadler J.E.;			

RT "Evolution of human von Willebrand factor: cDNA sequence
RT polymorphisms, repeated domains, and relationship to von Willebrand
RT antigen II.";
RL Biochem. Biophys. Res. Commun. 144:657-665(1987).
RN [4]
RN SEQUENCE OF 1-1400 FROM N.A.
RX MEDLINE-87004550; PubMed-3019665;
RA Verweij C.L., Diergaarde P.J., Hart M., Pannekoek H.;
RT "Full-length von Willebrand factor (vWF) cDNA encodes a highly
RT repetitive protein considerably larger than the mature vWF subunit.";
RL ENBO J. 5:1839-1847(1986).
RN [5]
RN ERRATUM.
RA Verweij C.L., Diergaarde P.J., Hart M., Pannekoek H.;
RL ENBO J. 5:3074-3074(1986).
RN [6]
RN SEQUENCE OF 764-2813.
RX MEDLINE-86269895; PubMed-3524673;
RA Titani K., Kumar S., Takio K., Ericsson L.H., Wade R.D., Ashida K.,
RA Walsh K.A., Choek M.W., Sadler J.E., Fujikawa K.;
RT "Amino acid sequence of human von Willebrand factor.";
RL Biochemistry 25:3171-3184(1986).
RN [7]
RN SEQUENCE OF 781-1424 FROM N.A.
RX MEDLINE-86269894; PubMed-3488076;
RA "cDNA sequences for human von Willebrand factor reveal five types of
RT repeated domains and five possible protein sequence polymorphisms.";
RL Biochemistry 25:3164-3171(1986).
RN [8]
RN SEQUENCE OF 764-873 AND 1289-2813 FROM N.A.
RX MEDLINE-86016708; PubMed-2864688;
RA Sadler J.E., Shelton-Inloes B.B., Sorace J.M., Harlan J.M.,
RA Titani K., Davie E.W.;
RT "Cloning and characterization of two cDNAs coding for human von
RT Willebrand factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:6394-6398(1985).
RN [9]
RN SEQUENCE OF 990-1947 FROM N.A.
RX MEDLINE-91105089; PubMed-1988024;
RA Mancuso D.J., Tuley E.A., Westfield L.A., Lester-Mancuso T.L.,
RA Le Beau M.M., Sorace J.M., Sadler J.E.;
RT "Human von Willebrand factor gene and pseudogene: structural analysis
RT and differentiation by polymerase chain reaction.";
RL Biochemistry 30:253-269(1991).
RN [10]
RN SEQUENCE OF 2731-2813 FROM N.A.
RX MEDLINE-85269603; PubMed-3875078;
RA Verweij C.L., de Vries C.J.M., Distel B., van Zonneveld A.-J.,
RA Geurts van Kessel A., van Mourik J.A., Pannekoek H.;
RT "Construction of cDNA coding for human von Willebrand factor using
RT antibody probes for colony-screening and mapping of the chromosomal
RT gene.";
RL Nucleic Acids Res. 13:4699-4717(1985).
RN [11]
RN SEQUENCE OF 1-177 FROM N.A.
RX MEDLINE-88111704; PubMed-2828057;
RA Bonthron D., Orkin S.H.;
RT "The human von Willebrand factor gene. Structure of the 5' region.";
RL Eur. J. Biochem. 171:51-57(1988).
RN [12]
RN SEQUENCE OF 2621-2813 FROM N.A.
RX MEDLINE-85244588; PubMed-3874428;
RA Ginsburg D., Handin R.I., Bonthron D.T., Donlon T.A., Bruns G.A.P.,
RA Latt S.A., Orkin S.H.;
RT "Human von Willebrand factor (vWF): isolation of complementary DNA
RT (cDNA) clones and chromosomal localization.";
RL Science 228:1401-1406(1985).
RN [13]
RN SEQUENCE OF 2731-2813 FROM N.A.
RX MEDLINE-85201687; PubMed-3873280;
RA Lynch D.C., Zimmerman T.S., Collins C.J., Brown M., Morin M.J.,
RA Ling E.H., Livingston D.M.;

RT "Molecular cloning of cDNA for human von Willebrand factor:
RT authentication by a new method.";
RL Cell 41:49-56(1985).
RN [14]
RN REVISIONS.
RA Lynch D.C.;
RL Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.
RN [15]
RN SEQUENCE OF 2731-2813 FROM N.A.
RX MEDLINE-87260814; PubMed-3496594;
RA Collins C.J., Underdahl J.P., Levene R.B., Ravera C.P.,
RA Morin M.J., Dombalagian M.J., Ricca G., Livingston D.M.,
RA Lynch D.C.;
RT "Molecular cloning of the human gene for von Willebrand factor and
RT identification of the transcription initiation site.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4393-4397(1987).
RN [16]
RN DISULFIDE BONDS.
RX MEDLINE-88163465; PubMed-3502076;
RA Marti T., Rosselet S.J., Titani K., Walsh K.A.;
RT "Identification of disulfide-bridged substructures within human von
RT Willebrand factor.";
RL Biochemistry 26:8099-8109(1987).
RN [17]
RN STRUCTURE OF CARBOHYDRATES.
RX MEDLINE-86274702; PubMed-3089784;
RA Samor B., Michalski J.C., Debray H., Mazurier C., Goudemand M.,
RA van Halbeek H., Vliegthart J.F.G., Montreuil J.;
RT "Primary structure of a new tetraantennary glycan of the N-
RT acetylglucosaminic type isolated from human factor VIII/von
RT Willebrand factor.";
RL Eur. J. Biochem. 158:295-298(1986).
RN [18]
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1261-1468.
RX MEDLINE-98221174; PubMed-9553097;
RA Emsley J., Cruz M., Handin R., Liddington R.;
RT "Crystal structure of the von Willebrand factor A1 domain and
RT implications for the binding of platelet glycoprotein Ib.";
RL J. Biol. Chem. 273:10396-10401(1998).
RN [19]
RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 1685-1873.
RX MEDLINE-97472999; PubMed-9331419;
RA Huizinga E.G., Martijn van der Plas R., Kroon J., Sixma J.J., Gros P.;
RT "Crystal structure of the A3 domain of human von Willebrand factor:
RT implications for collagen binding.";
RL Structure 5:1147-1156(1997).
RN [20]
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 1686-1872.
RX MEDLINE-97460108; PubMed-9312128;
RA Bienkowska J., Cruz M., Atieno A., Handin R., Liddington R.;
RT "The von Willebrand factor A3 domain does not contain a metal ion-
RT dependent adhesion site motif.";
RL J. Biol. Chem. 272:25162-25167(1997).
RN [21]
RN VARIANTS TRP-1597 AND ASP-1607.
RX MEDLINE-89264495; PubMed-2786201;
RA Ginsburg D., Konkle B.A., Gill J.C., Montgomery R.R.,
RA Bockenstedt P.L., Johnson T.A., Yang A.Y.;
RT "Molecular basis of human von Willebrand disease: analysis of
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VARIANTS TRP-1306; CYS-1308 AND PRO-1613.
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VARIANTS TRP-1306; CYS-1308; MET-1316; GLN-1341 AND HIS-1399.
MEDLINE=91185602; PubMed=1672694;
Cooney K.A., Nicholas W.C., Bruck M.E., Bahou W.F., Shapiro A.D.,
Query Match      5.8%; Score 133.5; DB 1; Length 2813;
Best Local Similarity 21.4%; Pred No. 0.029;
Matches 78; Conservative 38; Mismatches 107; Indels 141; Gaps 19;
QY 44 GNCVP---CNQCGRGMELSKECGFGYGDAQCVTCRLHREKEDWGFOCKRCLCDCAVNR 100
|:||| | || | | | | :|: | | | | | | | |
DB 2246 GSCVPEEACTQC-----ICGEDGV----QHOFLEAW-VPDHQPCTCTCLSG 2286
QY 101 FOKANCSA----TSDA-ICGDCLPGFRKYTKLVGFQDMEC-----VPCGDP PPPPEPHCAS 151
|:| |:| | | | | | | | | | | | | | | | | |
DB 2287 -RKVNCTQCPCTAKAPCTCGLCEVARLQNADQCCPEYCVDPVSCDLPP---VPHGER 2342
QY 152 KVNVLKVTASTASSPRDTALAAVICSALATVLLALLLCVIYKRFMEKKFWSLSRSQDI 211
|:| |:| | | | | | | | | | | | | | | | | |
DB 2343 -----GLQPLTNGE-----CRPNF----- 2358
QY 212 QYNGSELCLDRPOLHEYAHACQCRDSYOTCGPVRLPSM----CCEE---ACSPNP 264
|:| |:| | | | | | | | | | | | | | | | | |
DB 2359 -----TCACRKE-----ECKRVSPSPCPPHR-LPTLRKTQCCDEYCACNCVN 2400
QY 265 ATLCGGVHASLASLARNAAGNAPGEMVPTFFGSILTOSIGCFSDANPL----- 310
|:| |:| | | | | | | | | | | | | | | | | |
DB 2401 STVCPLGYLASTATNDGC-----CTTTCLPKVCVHRSTIYPVGQFWBEGCDVCTCT 2454
QY 311 -MQPMGMDNISFCDSYP-----ELTGEDIHSINPELESSTSLDNSSQ 353
|:| |:| | | | | | | | | | | | | | | | | |
DB 2455 DMEDAVNGLVAQCQRPCDCSRSGFTYVLHEGECGRCLPSACEVVYSGPRGDSQSSW 2514
QY 354 DLVG 357
DB 2515 KSVG 2518

RESULT 15
TSPI_MOUSE
ID TSPI_MOUSE STANDARD; PRG; 1170 AA.
AC P35441;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE THROMBOSPONDIN 1 PRECURSOR.
GN THBS1 OR TSPI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
```

MEDLINE=92128941; PubMed=1774063;
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Jenkins N.A.;
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SEQUENCE FROM N.A.
MEDLINE=92147683; PubMed=1371115;
Laberty C.D., O'Rourke K., Wolf F.W., Katz R., Seldin M.F.,
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SEQUENCE OF 1-490 FROM N.A.
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the role of the first intron in human gene expression.";
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-!- FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL AND
CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINOGEN, FIBRONECTIN,
LAMININ AND TYPE V COLLAGEN.
-!- SUBUNIT: HOMOTRIMER, CROSS-LINKED BY DISULFIDE BONDS.
-!- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
-!- SIMILARITY: CONTAINS 1 VWFC DOMAIN.
-!- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 3 TYPE-1 TSP REPEATS AND 7 TYPE-3 TSP REPEATS
(WHICH BIND CALCIUM).

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EMBL; M62470; AAA50611.1; JOINED.
EMBL; M62450; AAA50611.1; JOINED.
EMBL; M62451; AAA50611.1; JOINED.
EMBL; M62452; AAA50611.1; JOINED.
EMBL; M62453; AAA50611.1; JOINED.
EMBL; M62454; AAA50611.1; JOINED.
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EMBL; M87276; AAA53063.1; -
EMBL; J05606; AAA40431.1; -
EMBL; J05605; AAA40431.1; JOINED.
PIR; A40558; A40558.
PIR; B42587; B42587.
PIR; A37905; A37905.
HSSP; P35555; 1EMO.
MGD; MGI:98737; THBS1.
INTERPRO; IPR000561; -
INTERPRO; IPR000884; -
INTERPRO; IPR001007; -
PFAM; PF00008; EGF; 2.
PFAM; PF00090; tsp; 1; 3.
PFAM; PF00093; vwc; 1.

